



SEQUENCE LISTING

<110> Yumin, Tao
Gordon-Kamm, William
Shen, Bo
Lowe, Keith
Danilevskaya, Olga
Mahajan, Pramod
Rafalski, Jan Antoni
Sakai, Hajime
Klein, Theodore

<120> Transcriptional Regulatory Nucleic
Acids, Polypeptides, and Methods of Use Thereof

<130> 1288R

<150> 10/005,057

<151> 2001-12-04

<150> 60/251,555

<151> 2000-12-06

<160> 43

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1874

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (3)...(1655)

<400> 1

ac gag aat gat gaa tct cgc caa att cat tat gac gaa gct gca att	47
Glu Asn Asp Glu Ser Arg Gln Ile His Tyr Asp Glu Ala Ala Ile	
1 5 10 15	
 gag agg ttg tta gac cgt gat caa gtt gac ggt gat gaa tct gtg gaa	95
Glu Arg Leu Leu Asp Arg Asp Gln Val Asp Gly Asp Glu Ser Val Glu	
20 25 30	
 gat gaa gaa gaa gat gga ttc tta aaa gga ttc aag gtt gca aac ttt	143
Asp Glu Glu Glu Asp Gly Phe Leu Lys Gly Phe Lys Val Ala Asn Phe	
35 40 45	
 gaa tat atc gat gag gca aag gct cag gca gaa aaa gag gag gca cgg	191
Glu Tyr Ile Asp Glu Ala Lys Ala Gln Ala Glu Lys Glu Glu Ala Arg	
50 55 60	

aga aag gct gca gct gag gct gaa aat tct gaa aga aac tac tgg gat	239
Arg Lys Ala Ala Ala Glu Ala Glu Asn Ser Glu Arg Asn Tyr Trp Asp	
65 70 75	
gaa cta ttg aag gat aga tat gat gta cag aaa gtt gaa gaa cat act	287
Glu Leu Leu Lys Asp Arg Tyr Asp Val Gln Lys Val Glu Glu His Thr	
80 85 90 95	
gct atg gga aaa ggg aaa aga agc cgc aaa cag atg gct gcc gct gat	335
Ala Met Gly Lys Gly Lys Arg Ser Arg Lys Gln Met Ala Ala Ala Asp	
100 105 110	
gaa gat gac att cat gat tta agt tcc gaa gat gag gat tac tca ttg	383
Glu Asp Asp Ile His Asp Leu Ser Ser Glu Asp Glu Asp Tyr Ser Leu	
115 120 125	
gag gat gac att tca gat aat gac aca agt ttg caa gga aat att tct	431
Glu Asp Asp Ile Ser Asp Asn Asp Thr Ser Leu Gln Gly Asn Ile Ser	
130 135 140	
ggg aag agg gga caa tat tct aag aga aaa tca cgt aat gtt gat tct	479
Gly Lys Arg Gly Gln Tyr Ser Lys Arg Lys Ser Arg Asn Val Asp Ser	
145 150 155	
att cca ttg atg gag ggc gaa gga cgt acc ttg aga gtt ctt gga ttc	527
Ile Pro Leu Met Glu Gly Glu Gly Arg Thr Leu Arg Val Leu Gly Phe	
160 165 170 175	
aac cat gct caa cga gca atg ttc cta cag aca ctc aat aga ttc ggt	575
Asn His Ala Gln Arg Ala Met Phe Leu Gln Thr Leu Asn Arg Phe Gly	
180 185 190	
ttt cag aat tat gac tgg aaa gag tat ctt cct cgt ctt aaa gga aaa	623
Phe Gln Asn Tyr Asp Trp Lys Glu Tyr Leu Pro Arg Leu Lys Gly Lys	
195 200 205	
agt gtc gag gaa atc cag aga tat gct gaa ctt gtc atg gca cat ctt	671
Ser Val Glu Glu Ile Gln Arg Tyr Ala Glu Leu Val Met Ala His Leu	
210 215 220	
gtt gaa gaa att aat gat tct gac tat ttt tca gat ggc gtt cca aag	719
Val Glu Glu Ile Asn Asp Ser Asp Tyr Phe Ser Asp Gly Val Pro Lys	
225 230 235	
gaa atg atg cgt gtt gat gat gta cta gtc agg ata gca aac ata tcc	767
Glu Met Met Arg Val Asp Asp Val Leu Val Arg Ile Ala Asn Ile Ser	
240 245 250 255	
ctt atc gag gag aag atg gct gcc aca gga cca gga aaa att aca aac	815
Leu Ile Glu Glu Lys Met Ala Ala Thr Gly Pro Gly Lys Ile Thr Asn	
260 265 270	
att ttt cct aat tac ttg ctc tat gag ttc caa ggc tta tct ggt gga	863
Ile Phe Pro Asn Tyr Leu Leu Tyr Glu Phe Gln Gly Leu Ser Gly Gly	
275 280 285	

aga ata tgg aaa gcg gag cat gat cta ctg tta ctg aga ggc ata ctg Arg Ile Trp Lys Ala Glu His Asp Leu Leu Leu Leu Arg Gly Ile Leu 290 295 300	911
aag cat gga tat gca agg tgg cag tat ata tca gat gac aga gag aat Lys His Gly Tyr Ala Arg Trp Gln Tyr Ile Ser Asp Asp Arg Glu Asn 305 310 315	959
ggg ctt ttt gag gct gca cga cga gag ctg cat ctc cct tcg gtt aat Gly Leu Phe Glu Ala Ala Arg Arg Glu Leu His Leu Pro Ser Val Asn 320 325 330 335	1007
gaa ata att ggt gct cag ttg aac gag gca aat ggg aat ttg gaa ggt Glu Ile Ile Gly Ala Gln Leu Asn Glu Ala Asn Gly Asn Leu Glu Gly 340 345 350	1055
gca cag gaa ggc caa gcg aac aca aca agc atg tcg cat tac aag gag Ala Gln Glu Gly Gln Ala Asn Thr Thr Ser Met Ser His Tyr Lys Glu 355 360 365	1103
atc cag aga aag ata gtt gag ttc ttg aga aag aga tat cat ctt atg Ile Gln Arg Lys Ile Val Glu Phe Leu Arg Lys Arg Tyr His Leu Met 370 375 380	1151
gag aga gcc ttg aat ctg gaa tat gct gtg ata aag aaa aaa att cct Glu Arg Ala Leu Asn Leu Glu Tyr Ala Val Ile Lys Lys Lys Ile Pro 385 390 395	1199
gtt cct gat gat att act gaa caa ggt gtt cca gca gga cat gct ccg Val Pro Asp Asp Ile Thr Glu Gln Gly Val Pro Ala Gly His Ala Pro 400 405 410 415	1247
ctt att cca gat atc agt gaa ctg ttg cgg gaa ttg ccc aat ctt gag Leu Ile Pro Asp Ile Ser Glu Leu Leu Arg Glu Leu Pro Asn Leu Glu 420 425 430	1295
cca att tct acc aat gaa ttg att tct gag ggc aca gct ggt cag tta Pro Ile Ser Thr Asn Glu Leu Ile Ser Glu Gly Thr Ala Gly Gln Leu 435 440 445	1343
caa gtt ccc cat ctc tac aat aag atg tgt gga gtg ctt gaa gag agt Gln Val Pro His Leu Tyr Asn Lys Met Cys Gly Val Leu Glu Glu Ser 450 455 460	1391
ggg gct tat gcg ctc agt tcc ttc ttt gga gac aag tcc gca tct tct Gly Ala Tyr Ala Leu Ser Ser Phe Phe Gly Asp Lys Ser Ala Ser Ser 465 470 475	1439
act ttg gcc aat agc ctt cga cag ttt gaa act gtg tgt gag aat gtc Thr Leu Ala Asn Ser Leu Arg Gln Phe Glu Thr Val Cys Glu Asn Val 480 485 490 495	1487
gtc gag gcc tta cga cca cac caa aat ggt act gcc agt gcc atc aaa Val Glu Ala Leu Arg Pro His Gln Asn Gly Thr Ala Ser Ala Ile Lys 500 505 510	1535

gag gaa ttg gta gat gca gcc acc aaa gca gca gca gca gca gct cct 1583
Glu Glu Leu Val Asp Ala Ala Thr Lys Ala Ala Ala Ala Ala Ala Pro
515 520 525

aag gcg gac atg gaa atc gat ggt tgatttgtag gttccagagt ggcaagaaag 1685
Lys Ala Asp Met Glu Ile Asp Gly
545 550

```
<210> 2
<211> 551
<212> PRT
<213> Zea mays
```



```

<221> primer_bind
<222> (1)...(23)

<400> 4
tcaaccatcg atttccatgt ccg                                     23

<210> 5
<211> 941
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (48)...(938)

<400> 5
gtcgcacccac gcgtccgcag gattctggga agctccacac cttggat atg cta cta      56
                                         Met Leu Leu
                                         1

cga cgc ctt cga gct gaa ggt cat cgt gtg ctt ctt ttt gct cag atg      104
Arg Arg Leu Arg Ala Glu Gly His Arg Val Leu Leu Phe Ala Gln Met
      5                      10                      15

act aaa atg ttg gac att ctt gag gat tac atg aat ttc aga aaa ttc      152
Thr Lys Met Leu Asp Ile Leu Glu Asp Tyr Met Asn Phe Arg Lys Phe
      20                      25                      30                      35

aag tat ttc aga ctt gat ggg tct tca gcc atc tca gac cgc cgt gac      200
Lys Tyr Phe Arg Leu Asp Gly Ser Ser Ala Ile Ser Asp Arg Arg Asp
                      40                      45                      50

atg gtc cga gat ttt cag aac agg aat gac ata ttt gtt ttc ttg tta      248
Met Val Arg Asp Phe Gln Asn Arg Asn Asp Ile Phe Val Phe Leu Leu
                      55                      60                      65

agc aca aga gct ggg ggg ctt ggt att aat ttg act gct gct gat act      296
Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala Ala Asp Thr
                      70                      75                      80

gtt att ttt tat gaa att gac tgg aat cca aca caa gac cag cag gca      344
Val Ile Phe Tyr Glu Ile Asp Trp Asn Pro Thr Gln Asp Gln Gln Ala
      85                      90                      95

atg gat aga aca cac aga ctt ggt caa aca aag gag gta act gtg tac      392
Met Asp Arg Thr His Arg Leu Gly Gln Thr Lys Glu Val Thr Val Tyr
      100                      105                      110                      115

agg ctt ata tgc aaa gat acc att gag gag aaa ata ttg caa aga gca      440
Arg Leu Ile Cys Lys Asp Thr Ile Glu Glu Lys Ile Leu Gln Arg Ala
                      120                      125                      130

aag cag aaa aat gca gtg caa gag tta gtt atg aag ggg aaa cat gtc      488
Lys Gln Lys Asn Ala Val Gln Glu Leu Val Met Lys Gly Lys His Val
                      135                      140                      145

```

caa gac gat cat ttg atg aga caa gag gat gtt gtt tca tta ctt att Gln Asp Asp His Leu Met Arg Gln Glu Asp Val Val Ser Leu Leu Ile 150 155 160	536
gat gac aca cag att gca cac aag ttg aaa gaa ata tcc atg cag gcg Asp Asp Thr Gln Ile Ala His Lys Leu Lys Glu Ile Ser Met Gln Ala 165 170 175	584
aag gat cga caa aag agg aga cga gcg aag ggc atc aag gtt gac aaa Lys Asp Arg Gln Lys Arg Arg Arg Ala Lys Gly Ile Lys Val Asp Lys 180 185 190 195	632
gaa gga gat ttg acg ctc gaa gac ttg gat gat gct act gca gaa gct Glu Gly Asp Leu Thr Leu Glu Asp Leu Asp Asp Ala Thr Ala Glu Ala 200 205 210	680
gta gat caa gac aaa acg acc agc aaa aag aaa aag agc tcc cac aag Val Asp Gln Asp Lys Thr Thr Ser Lys Lys Lys Ser Ser His Lys 215 220 225	728
aaa cat acg aat act cat gat aat gac aat ata gac aag aat gga gag Lys His Thr Asn Thr His Asp Asn Asp Asn Ile Asp Lys Asn Gly Glu 230 235 240	776
gcc gat gtg gga gat cat ccg ggg agt agt aac aca gaa aac gaa cag Ala Asp Val Gly Asp His Pro Gly Ser Ser Asn Thr Glu Asn Glu Gln 245 250 255	824
atg ccc gaa tca aga cct aaa aga tca aaa agg ctg atg aag agc att Met Pro Glu Ser Arg Pro Lys Arg Ser Lys Arg Leu Met Lys Ser Ile 260 265 270 275	872
act gat gac aag gaa cta gct gct gct gcg gat cat gag aaa ccg gta Thr Asp Asp Lys Glu Leu Ala Ala Ala Ala Asp His Glu Lys Pro Val 280 285 290	920
aat gaa gcg gaa aat cac tga Asn Glu Ala Glu Asn His 295	941

<210> 6

<211> 297

<212> PRT

<213> Zea mays

<220>

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Any Amino Acid

<400> 6

Met	Leu	Leu	Arg	Arg	Leu	Arg	Ala	Glu	Gly	His	Arg	Val	Leu	Leu	Phe
1				5					10					15	
Ala	Gln	Met	Thr	Lys	Met	Leu	Asp	Ile	Leu	Glu	Asp	Tyr	Met	Asn	Phe
			20					25					30		

Arg Lys Phe Lys Tyr Phe Arg Leu Asp Gly Ser Ser Ala Ile Ser Asp
 35 40 45
 Arg Arg Asp Met Val Arg Asp Phe Gln Asn Arg Asn Asp Ile Phe Val
 50 55 60
 Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala
 65 70 75 80
 Ala Asp Thr Val Ile Phe Tyr Glu Ile Asp Trp Asn Pro Thr Gln Asp
 85 90 95
 Gln Gln Ala Met Asp Arg Thr His Arg Leu Gly Gln Thr Lys Glu Val
 100 105 110
 Thr Val Tyr Arg Leu Ile Cys Lys Asp Thr Ile Glu Glu Lys Ile Leu
 115 120 125
 Gln Arg Ala Lys Gln Lys Asn Ala Val Gln Glu Leu Val Met Lys Gly
 130 135 140
 Lys His Val Gln Asp Asp His Leu Met Arg Gln Glu Asp Val Val Ser
 145 150 155 160
 Leu Leu Ile Asp Asp Thr Gln Ile Ala His Lys Leu Lys Glu Ile Ser
 165 170 175
 Met Gln Ala Lys Asp Arg Gln Lys Arg Arg Arg Ala Lys Gly Ile Lys
 180 185 190
 Val Asp Lys Glu Gly Asp Leu Thr Leu Glu Asp Leu Asp Asp Ala Thr
 195 200 205
 Ala Glu Ala Val Asp Gln Asp Lys Thr Thr Ser Lys Lys Lys Lys Ser
 210 215 220
 Ser His Lys Lys His Thr Asn Thr His Asp Asn Asp Asn Ile Asp Lys
 225 230 235 240
 Asn Gly Glu Ala Asp Val Gly Asp His Pro Gly Ser Ser Asn Thr Glu
 245 250 255
 Asn Glu Gln Met Pro Glu Ser Arg Pro Lys Arg Ser Lys Arg Leu Met
 260 265 270
 Lys Ser Ile Thr Asp Asp Lys Glu Leu Ala Ala Ala Ala Asp His Glu
 275 280 285
 Lys Pro Val Asn Glu Ala Glu Asn His
 290 295

<210> 7
 <211> 22
 <212> DNA
 <213> Zea mays

<220>
 <221> primer_bind
 <222> (1)...(22)

<400> 7
 aagctccaca ccttgatat gc

22

<210> 8
 <211> 23
 <212> DNA
 <213> Zea mays
 <220>
 <221> primer_bind
 <222> (1)...(23)

<400> 8

tcatgggctc agtgattttc cgc

23

<210> 9

<211> 1913

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (3)...(1910)

<400> 9

ca cac tta ata att gct cca aaa gca gta tta cca aat tgg tct aac 47

His Leu Ile Ile Ala Pro Lys Ala Val Leu Pro Asn Trp Ser Asn

1 5 10 15

gaa ttc aaa acc tgg gct ccc agt att ggg aca att ctg tat gat ggt 95

Glu Phe Lys Thr Trp Ala Pro Ser Ile Gly Thr Ile Leu Tyr Asp Gly

20 25 30

cgt cca gaa gag agg aag ctt tta agg gaa aag aat ttt gat gga ttg 143

Arg Pro Glu Glu Arg Lys Leu Leu Arg Glu Lys Asn Phe Asp Gly Leu

35 40 45

caa ttt aat gtt ttg ctc acg cat tat gac ttg ata ctg aaa gat aag 191

Gln Phe Asn Val Leu Leu Thr His Tyr Asp Leu Ile Leu Lys Asp Lys

50 55 60

aag ttc cta aag aaa gtt cac tgg cat tat ttg att gtt gat gaa gga 239

Lys Phe Leu Lys Lys Val His Trp His Tyr Leu Ile Val Asp Glu Gly

65 70 75

cat cgt ctg aaa aat cat gaa tgt gct ctt gct cgc aca cta gtt tca 287

His Arg Leu Lys Asn His Glu Cys Ala Leu Ala Arg Thr Leu Val Ser

80 85 90 95

gga tat cag atc cgc cgc aga cta ctt tta act ggc act cca atc caa 335

Gly Tyr Gln Ile Arg Arg Arg Leu Leu Leu Thr Gly Thr Pro Ile Gln

100 105 110

aat agc cta caa gaa ctg tgg tct ttg ctt aac ttt att ctg ccc aat 383

Asn Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe Ile Leu Pro Asn

115 120 125

att ttt aat tca tct cag aat ttt gag gaa tgg ttt aat gca cca ttt 431

Ile Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe Asn Ala Pro Phe

130 135 140

gca tgt gat gtt agt ctt aat gat gag gaa cag cta tta atc ata cat 479

Ala Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu Leu Ile Ile His

145 150 155

cgt ctg cat caa gtt ttg cgt cca ttt ttg ctg agg agg aaa aaa gat 527

Arg Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg Arg Lys Lys Asp

160 165 170 175

gaa gtg gaa aaa tat ctc cct gtc aaa aca caa gta att ctc aag tgt	575
Glu Val Glu Lys Tyr Leu Pro Val Lys Thr Gln Val Ile Leu Lys Cys	
180 185 190	
gat atg tct gct tgg caa aaa gca tac tat gaa caa gtc aca agc agg	623
Asp Met Ser Ala Trp Gln Lys Ala Tyr Tyr Glu Gln Val Thr Ser Arg	
195 200 205	
gaa aag gtt gca cta gga ttt ggg ctc aga tca aag gct ctg cag aat	671
Glu Lys Val Ala Leu Gly Phe Gly Leu Arg Ser Lys Ala Leu Gln Asn	
210 215 220	
ctg tca atg caa ctt agg aaa tgt tgc aac cac ccc tat cta ttt gta	719
Leu Ser Met Gln Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Phe Val	
225 230 235	
gag cac tac aac atg tac cag cgg gag gaa att gtt aga gca tca ggg	767
Glu His Tyr Asn Met Tyr Gln Arg Glu Glu Ile Val Arg Ala Ser Gly	
240 245 250 255	
aag ttt gaa ttg ctt gat cgt cta ctt cca aaa ctg cag aga gct ggt	815
Lys Phe Glu Leu Leu Asp Arg Leu Leu Pro Lys Leu Gln Arg Ala Gly	
260 265 270	
cac agg gtt ctg ctt ttc tct cag atg acg aaa ctg ctt gat gtt tta	863
His Arg Val Leu Leu Phe Ser Gln Met Thr Lys Leu Leu Asp Val Leu	
275 280 285	
gaa ata tat ttg caa atg tac aat ttc aag tac atg agg ctt gat gga	911
Glu Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met Arg Leu Asp Gly	
290 295 300	
tcc acg aag act gaa gaa cga ggg agg tta ctg gca gat ttt aat aag	959
Ser Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala Asp Phe Asn Lys	
305 310 315	
aag gat tcg gaa tat ttc atg ttt ctc ctc agc aca cgt gct gga gga	1007
Lys Asp Ser Glu Tyr Phe Met Phe Leu Leu Ser Thr Arg Ala Gly Gly	
320 325 330 335	
ctt ggg ttg aac ttg cag acg gcg gac act gtc att ata ttt gat agt	1055
Leu Gly Leu Asn Leu Gln Thr Ala Asp Thr Val Ile Ile Phe Asp Ser	
340 345 350	
gac tgg aac cct caa atg gac caa caa gct gaa gac cgt gcc cat cgt	1103
Asp Trp Asn Pro Gln Met Asp Gln Gln Ala Glu Asp Arg Ala His Arg	
355 360 365	
ata ggc aga aga atg aag tgc gtg tgt ttg ttc ttg tta gtg tcg gct	1151
Ile Gly Arg Arg Met Lys Cys Val Cys Leu Phe Leu Leu Val Ser Ala	
370 375 380	
cca ttg aag aag aga tcc tgg acc gtg caa aac aaa aga tgg gta tcg	1199
Pro Leu Lys Lys Arg Ser Trp Thr Val Gln Asn Lys Arg Trp Val Ser	
385 390 395	

atg	caa	aag	tta	ctc	cag	gct	ggg	ttg	ttt	aac	aca	act	tcc	aca	gca	1247
Met	Gln	Lys	Leu	Leu	Gln	Ala	Gly	Leu	Phe	Asn	Thr	Thr	Ser	Thr	Ala	
400					405					410					415	
cag	gac	aga	cga	gca	ttg	ctg	cag	gag	atc	ctt	agg	agg	ggg	aca	agc	1295
Gln	Asp	Arg	Arg	Ala	Leu	Leu	Gln	Glu	Ile	Leu	Arg	Arg	Gly	Thr	Ser	
				420					425					430		
tcg	ctg	gga	aca	gat	atc	ccc	agt	gag	cgc	gag	ata	aat	cgt	ttg	gct	1343
Ser	Leu	Gly	Thr	Asp	Ile	Pro	Ser	Glu	Arg	Glu	Ile	Asn	Arg	Leu	Ala	
			435					440					445			
gca	cga	act	gat	gaa	gaa	ttc	tgg	ttg	ttt	gag	aag	atg	gat	gaa	gaa	1391
Ala	Arg	Thr	Asp	Glu	Glu	Phe	Trp	Leu	Phe	Glu	Lys	Met	Asp	Glu	Glu	
		450					455					460				
agg	agg	ctt	aga	gaa	aac	tac	aaa	tct	aga	ctt	atg	gat	ggg	aat	gag	1439
Arg	Arg	Leu	Arg	Glu	Asn	Tyr	Lys	Ser	Arg	Leu	Met	Asp	Gly	Asn	Glu	
	465					470					475					
gtt	cca	gat	tgg	gta	ttc	gcc	aac	aat	gat	tta	ccc	aag	aga	acc	gtg	1487
Val	Pro	Asp	Trp	Val	Phe	Ala	Asn	Asn	Asp	Leu	Pro	Lys	Arg	Thr	Val	
480					485					490					495	
gca	gat	gag	ttc	cag	aat	ata	atg	gtc	ggt	gcg	aag	cga	cgt	aga	aag	1535
Ala	Asp	Glu	Phe	Gln	Asn	Ile	Met	Val	Gly	Ala	Lys	Arg	Arg	Arg	Lys	
				500					505					510		
gag	gtt	gtc	tat	tca	gac	tct	ttc	ggt	gat	cag	tgg	atg	aaa	tcc	gat	1583
Glu	Val	Val	Tyr	Ser	Asp	Ser	Phe	Gly	Asp	Gln	Trp	Met	Lys	Ser	Asp	
			515					520					525			
gag	gga	ttt	gaa	gac	att	cca	aag	gcg	act	cag	agg	tcg	aag	aag	act	1631
Glu	Gly	Phe	Glu	Asp	Ile	Pro	Lys	Ala	Thr	Gln	Arg	Ser	Lys	Lys	Thr	
		530					535					540				
gct	tac	tca	tct	gac	atc	caa	gtt	gag	ttt	agt	gaa	agg	agg	aaa	aga	1679
Ala	Tyr	Ser	Ser	Asp	Ile	Gln	Val	Glu	Phe	Ser	Glu	Arg	Arg	Lys	Arg	
	545					550					555					
cct	agg	tct	gta	gaa	aac	agc	gca	gac	ggt	gtg	agc	aac	ccg	acg	tgg	1727
Pro	Arg	Ser	Val	Glu	Asn	Ser	Ala	Asp	Gly	Val	Ser	Asn	Pro	Thr	Trp	
560					565					570					575	
acg	cct	gac	aaa	gga	agg	gct	gga	gtt	tca	tca	tac	agc	aag	gac	gag	1775
Thr	Pro	Asp	Lys	Gly	Arg	Ala	Gly	Val	Ser	Ser	Tyr	Ser	Lys	Asp	Glu	
				580				585						590		
act	gaa	gat	gat	ggc	gaa	gac	gaa	gtc	att	act	agc	ggc	tta	caa	aag	1823
Thr	Glu	Asp	Asp	Gly	Glu	Asp	Glu	Val	Ile	Thr	Ser	Gly	Leu	Gln	Lys	
			595					600					605			
gga	aac	agt	ttc	aca	tgg	aat	acc	cta	gga	aga	aga	agg	tca	agc	cac	1871
Gly	Asn	Ser	Phe	Thr	Trp	Asn	Thr	Leu	Gly	Arg	Arg	Arg	Ser	Ser	His	
		610					615					620				

ttc agt tcg tca tcg gac tcg aga ggg cgc cca aca ttc taa
Phe Ser Ser Ser Ser Asp Ser Arg Gly Arg Pro Thr Phe
625 630 635

1913

<210> 10
<211> 636
<212> PRT
<213> Zea mays

<400> 10
His Leu Ile Ile Ala Pro Lys Ala Val Leu Pro Asn Trp Ser Asn Glu
1 5 10 15
Phe Lys Thr Trp Ala Pro Ser Ile Gly Thr Ile Leu Tyr Asp Gly Arg
20 25 30
Pro Glu Glu Arg Lys Leu Leu Arg Glu Lys Asn Phe Asp Gly Leu Gln
35 40 45
Phe Asn Val Leu Leu Thr His Tyr Asp Leu Ile Leu Lys Asp Lys Lys
50 55 60
Phe Leu Lys Lys Val His Trp His Tyr Leu Ile Val Asp Glu Gly His
65 70 75 80
Arg Leu Lys Asn His Glu Cys Ala Leu Ala Arg Thr Leu Val Ser Gly
85 90 95
Tyr Gln Ile Arg Arg Arg Leu Leu Leu Thr Gly Thr Pro Ile Gln Asn
100 105 110
Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe Ile Leu Pro Asn Ile
115 120 125
Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe Asn Ala Pro Phe Ala
130 135 140
Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu Leu Ile Ile His Arg
145 150 155 160
Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg Arg Lys Lys Asp Glu
165 170 175
Val Glu Lys Tyr Leu Pro Val Lys Thr Gln Val Ile Leu Lys Cys Asp
180 185 190
Met Ser Ala Trp Gln Lys Ala Tyr Tyr Glu Gln Val Thr Ser Arg Glu
195 200 205
Lys Val Ala Leu Gly Phe Gly Leu Arg Ser Lys Ala Leu Gln Asn Leu
210 215 220
Ser Met Gln Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Phe Val Glu
225 230 235 240
His Tyr Asn Met Tyr Gln Arg Glu Glu Ile Val Arg Ala Ser Gly Lys
245 250 255
Phe Glu Leu Leu Asp Arg Leu Leu Pro Lys Leu Gln Arg Ala Gly His
260 265 270
Arg Val Leu Leu Phe Ser Gln Met Thr Lys Leu Leu Asp Val Leu Glu
275 280 285
Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met Arg Leu Asp Gly Ser
290 295 300
Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala Asp Phe Asn Lys Lys
305 310 315 320
Asp Ser Glu Tyr Phe Met Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu
325 330 335
Gly Leu Asn Leu Gln Thr Ala Asp Thr Val Ile Ile Phe Asp Ser Asp
340 345 350
Trp Asn Pro Gln Met Asp Gln Gln Ala Glu Asp Arg Ala His Arg Ile

<400> 12
ttagaatggtt gggcgccctc t 21

<210> 13
<211> 1463
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)...(1460)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G; Xaa = Any Amino Acid

<400> 13
gt cga ccc acg cgt ccg cca gaa gag cgg aac cat ata agg gac aat 47
Arg Pro Thr Arg Pro Pro Glu Glu Arg Asn His Ile Arg Asp Asn
1 5 10 15

ttg ctg caa cct ggg aaa ttt gat gtg tgt gtg act agt ttt gaa atg 95
Leu Leu Gln Pro Gly Lys Phe Asp Val Cys Val Thr Ser Phe Glu Met
20 25 30

gca atc aaa gaa aaa tct gcg ttg agg cgc ttc agc tgg cgc tac ata 143
Ala Ile Lys Glu Lys Ser Ala Leu Arg Arg Phe Ser Trp Arg Tyr Ile
35 40 45

atc att gat gaa gct cac cgg ata aaa aat gaa aat tct ctt cta tca 191
Ile Ile Asp Glu Ala His Arg Ile Lys Asn Glu Asn Ser Leu Leu Ser
50 55 60

aag act atg agg att tac aac act aat tat cgt ctc ctc atc aca ggc 239
Lys Thr Met Arg Ile Tyr Asn Thr Asn Tyr Arg Leu Leu Ile Thr Gly
65 70 75

act cca ctc cag aat aat ctc cat gag ctc tgg gct ctc ctc aat ttc 287
Thr Pro Leu Gln Asn Asn Leu His Glu Leu Trp Ala Leu Leu Asn Phe
80 85 90 95

ttg cta cct gaa ata ttt agc tct gcg gag acc ttt gat gaa tgg ttt 335
Leu Leu Pro Glu Ile Phe Ser Ser Ala Glu Thr Phe Asp Glu Trp Phe
100 105 110

caa ata tct ggg gaa aat gat caa cag gag gtg gtg cag cag ctt cat 383
Gln Ile Ser Gly Glu Asn Asp Gln Gln Glu Val Val Gln Gln Leu His
115 120 125

aag gtt ctt cgc cca ttc ctt ctt agg agg ctc aag tct gat gta naa 431
Lys Val Leu Arg Pro Phe Leu Leu Arg Arg Leu Lys Ser Asp Val Xaa
130 135 140

aag ggc cta cct cca aag aaa gaa aca att ctt aaa gtt gga atg tct 479
Lys Gly Leu Pro Pro Lys Lys Glu Thr Ile Leu Lys Val Gly Met Ser

145	150	155	
cag atg caa aag cag tac tat cgt gct ctg ctt cag aag gat ttg gag Gln Met Gln Lys Gln Tyr Tyr Arg Ala Leu Leu Gln Lys Asp Leu Glu 160 165 170 175			527
gtt att aat gct ggt ggt gaa cgc aag cga ttg ctt aac att gcc atg Val Ile Asn Ala Gly Gly Glu Arg Lys Arg Leu Leu Asn Ile Ala Met 180 185 190			575
cag ttg cgc aag tgc tgc aac cat cca tat tta ttc caa gga gct gaa Gln Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Phe Gln Gly Ala Glu 195 200 205			623
cct ggg cca ccc tac aca act ggt gaa cat cta att gag aat gca gga Pro Gly Pro Pro Tyr Thr Thr Gly Glu His Leu Ile Glu Asn Ala Gly 210 215 220			671
aaa atg gtt cta ctt gat aaa ttg ctg ccc aag cta aag gag cgt gat Lys Met Val Leu Leu Asp Lys Leu Leu Pro Lys Leu Lys Glu Arg Asp 225 230 235			719
tcc aga gtc ctt att ttt tca cag atg acc agg ctt ttg gat atc ttg Ser Arg Val Leu Ile Phe Ser Gln Met Thr Arg Leu Leu Asp Ile Leu 240 245 250 255			767
gaa gat tat ctt atg tat agg gga tat cag tat tgt cga att gat gga Glu Asp Tyr Leu Met Tyr Arg Gly Tyr Gln Tyr Cys Arg Ile Asp Gly 260 265 270			815
aat aca ggt gga gaa gat cgt gat gca tcc att gaa gcc ttc aat agt Asn Thr Gly Gly Glu Asp Arg Asp Ala Ser Ile Glu Ala Phe Asn Ser 275 280 285			863
cca gga agt gag aag ttt gtt ttc tta ctt tca act agg gca ggt ggc Pro Gly Ser Glu Lys Phe Val Phe Leu Leu Ser Thr Arg Ala Gly Gly 290 295 300			911
ctt ggt atc aac ttg gcc act gct gat gtt gtg gtt ctc tat gac agc Leu Gly Ile Asn Leu Ala Thr Ala Asp Val Val Val Leu Tyr Asp Ser 305 310 315			959
gat tgg aat ccc caa gct gat ctg caa gct cag gac cgt gca cat aga Asp Trp Asn Pro Gln Ala Asp Leu Gln Ala Gln Asp Arg Ala His Arg 320 325 330 335			1007
ata ggt caa aaa gaa aga agt tca agt gtt ccg ctt ttg cac ttg agt Ile Gly Gln Lys Glu Arg Ser Ser Ser Val Pro Leu Leu His Leu Ser 340 345 350			1055
tca act att gag gaa aag gtg att gag aga gca tat aag aag cta gca Ser Thr Ile Glu Glu Lys Val Ile Glu Arg Ala Tyr Lys Lys Leu Ala 355 360 365			1103
ttg gat gct ttg gtt att cag caa gga cga ttg gca gag cag aaa act Leu Asp Ala Leu Val Ile Gln Gln Gly Arg Leu Ala Glu Gln Lys Thr			1151

370	375	380	
gtc aat aag gat gat ctt ctg caa atg gtg cgg ttt ggt gct gaa atg			1199
Val Asn Lys Asp Asp Leu Leu Gln Met Val Arg Phe Gly Ala Glu Met			
385	390	395	
ggt ttc agt tct aag gac agc aca ata act gat gag gac att gac cgt			1247
Val Phe Ser Ser Lys Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp Arg			
400	405	410	415
att ata gct aaa gga gag gag aca aca gca gaa ctt gat gcg aaa atg			1295
Ile Ile Ala Lys Gly Glu Glu Thr Thr Ala Glu Leu Asp Ala Lys Met			
	420	425	430
aaa aag ttc act gag gat gcc atc aaa ttt aag atg gat gat aat gct			1343
Lys Lys Phe Thr Glu Asp Ala Ile Lys Phe Lys Met Asp Asp Asn Ala			
	435	440	445
gaa ttg tat gac ttc gat gat gag aag gat gaa aac aag gtt gat ttc			1391
Glu Leu Tyr Asp Phe Asp Asp Glu Lys Asp Glu Asn Lys Val Asp Phe			
	450	455	460
aag aaa ctt gtt agt gat aac tgg att gag cca cct aga aga gaa agg			1439
Lys Lys Leu Val Ser Asp Asn Trp Ile Glu Pro Pro Arg Arg Glu Arg			
	465	470	475
aag nga aac tac tct gag tct tga			1463
Lys Xaa Asn Tyr Ser Glu Ser			
480	485		

<210> 14
 <211> 486
 <212> PRT
 <213> Zea mays

<220>
 <221> VARIANT
 <222> (0)...(0)
 <223> Xaa = Any Amino Acid

<400> 14

Arg	Pro	Thr	Arg	Pro	Pro	Glu	Glu	Arg	Asn	His	Ile	Arg	Asp	Asn	Leu
1				5					10					15	
Leu	Gln	Pro	Gly	Lys	Phe	Asp	Val	Cys	Val	Thr	Ser	Phe	Glu	Met	Ala
			20					25					30		
Ile	Lys	Glu	Lys	Ser	Ala	Leu	Arg	Arg	Phe	Ser	Trp	Arg	Tyr	Ile	Ile
	35						40					45			
Ile	Asp	Glu	Ala	His	Arg	Ile	Lys	Asn	Glu	Asn	Ser	Leu	Leu	Ser	Lys
	50					55					60				
Thr	Met	Arg	Ile	Tyr	Asn	Thr	Asn	Tyr	Arg	Leu	Leu	Ile	Thr	Gly	Thr
65					70					75				80	
Pro	Leu	Gln	Asn	Asn	Leu	His	Glu	Leu	Trp	Ala	Leu	Leu	Asn	Phe	Leu
			85						90					95	
Leu	Pro	Glu	Ile	Phe	Ser	Ser	Ala	Glu	Thr	Phe	Asp	Glu	Trp	Phe	Gln
			100					105					110		


```

<222> (1)...(23)

<400> 15
ccagaagagc ggaaccatat aag 23

<210> 16
<211> 23
<212> DNA
<213> Zea mays

<220>
<221> primer_bind
<222> (1)...(23)

<400> 16
ctcttctagg tggctcaatc cag 23

<210> 17
<211> 1645
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (2)...(1642)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G; Xaa = Any Amino Acid

<400> 17
a gca gat ggg aga aga tac atg atc cgc cgg aga cta ctt tta aca ggc 49
Ala Asp Gly Arg Arg Tyr Met Ile Arg Arg Arg Leu Leu Leu Thr Gly
1 5 10 15

act cct atc caa aac agc ctg caa gag ctc tgg tct ttg ctt aac ttc 97
Thr Pro Ile Gln Asn Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe
20 25 30

atc ctg ccc aat att ttt aat tca tcc cag aat ttt gag gaa tgg ttt 145
Ile Leu Pro Asn Ile Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe
35 40 45

aat gca cca ttt gca tgt gat gtc agt ctt aat gat gag gaa caa cta 193
Asn Ala Pro Phe Ala Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu
50 55 60

cta atc ata cat cgt ttg cat caa gtt ttg cgt cca ttc ttg ctg agg 241
Leu Ile Ile His Arg Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg
65 70 75 80

agg aag aaa gat gaa gta nag aaa tat ctc cct gtg aaa aca caa gta 289
Arg Lys Lys Asp Glu Val Xaa Lys Tyr Leu Pro Val Lys Thr Gln Val
85 90 95

att ctc aag tgt gac atg tct gct tgg caa aaa gca tac tac gaa caa 337

```

Ile	Leu	Lys	Cys	Asp	Met	Ser	Ala	Trp	Gln	Lys	Ala	Tyr	Tyr	Glu	Gln		
			100					105					110				
gtc	aca	agc	agg	gaa	aag	gtt	gcg	cta	gga	tat	ggg	atc	aga	aag	aag	385	
Val	Thr	Ser	Arg	Glu	Lys	Val	Ala	Leu	Gly	Tyr	Gly	Ile	Arg	Lys	Lys		
		115					120				125						
gct	ctg	caa	aat	ctg	tca	atg	caa	ctt	agg	aag	tgt	tgc	aat	cat	ccc	433	
Ala	Leu	Gln	Asn	Leu	Ser	Met	Gln	Leu	Arg	Lys	Cys	Cys	Asn	His	Pro		
	130					135				140							
tac	cta	ttc	gta	gag	cat	tat	aac	atg	tac	caa	cgg	gag	gaa	ata	gtt	481	
Tyr	Leu	Phe	Val	Glu	His	Tyr	Asn	Met	Tyr	Gln	Arg	Glu	Glu	Ile	Val		
145					150				155						160		
aga	gca	tcc	gga	aag	ttt	gaa	ttg	ctt	gat	cgt	cta	ctt	ccg	aaa	ttg	529	
Arg	Ala	Ser	Gly	Lys	Phe	Glu	Leu	Leu	Asp	Arg	Leu	Leu	Pro	Lys	Leu		
			165					170						175			
cag	aga	gct	ggg	cac	agg	gtt	tta	ctt	ttc	tct	cag	atg	aca	aaa	ttg	577	
Gln	Arg	Ala	Gly	His	Arg	Val	Leu	Leu	Phe	Ser	Gln	Met	Thr	Lys	Leu		
		180					185						190				
ctt	gac	gtt	tta	gaa	ata	tat	ttg	cag	atg	tac	aat	ttc	aag	tac	atg	625	
Leu	Asp	Val	Leu	Glu	Ile	Tyr	Leu	Gln	Met	Tyr	Asn	Phe	Lys	Tyr	Met		
	195						200				205						
agg	ctt	gat	gga	tcc	aca	aag	act	gaa	gaa	cgt	ggg	agg	tta	ctg	gca	673	
Arg	Leu	Asp	Gly	Ser	Thr	Lys	Thr	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Ala		
	210					215				220							
gat	ttt	aat	aag	aag	aat	tca	gaa	tat	ttc	atg	ttt	ctt	ctc	agc	aca	721	
Asp	Phe	Asn	Lys	Lys	Asn	Ser	Glu	Tyr	Phe	Met	Phe	Leu	Leu	Ser	Thr		
225					230				235						240		
cga	gcc	gga	ggg	ctt	gga	ttg	aac	ttg	cag	act	gca	gac	acc	gtc	att	769	
Arg	Ala	Gly	Gly	Leu	Gly	Leu	Asn	Leu	Gln	Thr	Ala	Asp	Thr	Val	Ile		
			245					250						255			
atc	ttt	gat	agt	gac	tggt	aac	cct	cag	atg	gac	caa	caa	gct	gag	gac	817	
Ile	Phe	Asp	Ser	Asp	Trp	Asn	Pro	Gln	Met	Asp	Gln	Gln	Ala	Glu	Asp		
		260					265						270				
cgt	gcc	cat	cgt	ata	ggg	caa	aag	aac	gaa	gta	cgt	gtg	ttt	gtt	ctt	865	
Arg	Ala	His	Arg	Ile	Gly	Gln	Lys	Asn	Glu	Val	Arg	Val	Phe	Val	Leu		
		275					280				285						
gtt	agc	gtt	ggg	tca	att	gaa	gaa	gag	ata	ttg	gat	cgt	gcg	aaa	cag	913	
Val	Ser	Val	Gly	Ser	Ile	Glu	Glu	Glu	Ile	Leu	Asp	Arg	Ala	Lys	Gln		
	290					295					300						
aag	atg	ggg	att	gat	gca	aaa	gta	atc	cag	gct	ggg	ttg	ttt	aac	acg	961	
Lys	Met	Gly	Ile	Asp	Ala	Lys	Val	Ile	Gln	Ala	Gly	Leu	Phe	Asn	Thr		
305					310				315						320		
acc	tcc	aca	gca	cag	gac	agg	cga	gca	ttg	ctg	cag	gag	ata	ctc	agg	1009	

Thr Ser Thr Ala Gln Asp Arg Arg Ala Leu Leu Gln Glu Ile Leu Arg	
325 330 335	
aga gga aca agc tca ctg gga acg gat atc ccc agt gaa cgt gag ata	1057
Arg Gly Thr Ser Ser Leu Gly Thr Asp Ile Pro Ser Glu Arg Glu Ile	
340 345 350	
aac cgc ttg gct gct cga aac gat gaa gaa ttc cgg ttg ttt gag aag	1105
Asn Arg Leu Ala Ala Arg Asn Asp Glu Glu Phe Arg Leu Phe Glu Lys	
355 360 365	
atg gat gaa gaa agg agg cta aag gag aac tac aaa tct aga ctt atg	1153
Met Asp Glu Glu Arg Arg Leu Lys Glu Asn Tyr Lys Ser Arg Leu Met	
370 375 380	
gat gga aat gag gtc cca gat tgg gtg ttt gcc aat gat aat gaa acc	1201
Asp Gly Asn Glu Val Pro Asp Trp Val Phe Ala Asn Asp Asn Glu Thr	
385 390 395 400	
tta cgc aag aaa acc gtg gca gat gaa ttc cgg aat ata att gtt ggt	1249
Leu Arg Lys Lys Thr Val Ala Asp Glu Phe Arg Asn Ile Ile Val Gly	
405 410 415	
tca aag aga cgt aga aag gag gtt gtc tat tcg gac tct ttt ggt gat	1297
Ser Lys Arg Arg Arg Lys Glu Val Val Tyr Ser Asp Ser Phe Gly Asp	
420 425 430	
cag tgg atg aaa tcc gac gag gga ttt gaa gag att gca aag atg act	1345
Gln Trp Met Lys Ser Asp Glu Gly Phe Glu Glu Ile Ala Lys Met Thr	
435 440 445	
cca agg gtg aag cga act gct tat tcg cct gac att caa gtt gag tac	1393
Pro Arg Val Lys Arg Thr Ala Tyr Ser Pro Asp Ile Gln Val Glu Tyr	
450 455 460	
aat gaa agg agg aaa agg ccc aag tct gtg gaa aac agc gca gat ggc	1441
Asn Glu Arg Arg Lys Arg Pro Lys Ser Val Glu Asn Ser Ala Asp Gly	
465 470 475 480	
gca agc aac cca aca cgg aca ccc gac aaa gga agg gct gga gtt tca	1489
Ala Ser Asn Pro Thr Arg Thr Pro Asp Lys Gly Arg Ala Gly Val Ser	
485 490 495	
tca tac agc aag gat gag acc gaa gat gat ggt gaa gac gaa gtc atc	1537
Ser Tyr Ser Lys Asp Glu Thr Glu Asp Asp Gly Glu Asp Glu Val Ile	
500 505 510	
acc agt ggc tta cag aag ggt aac agt ttc aca tgg aag acc ctt gga	1585
Thr Ser Gly Leu Gln Lys Gly Asn Ser Phe Thr Trp Lys Thr Leu Gly	
515 520 525	
aga aaa agg tca agc cac tta agt tcg tcg tcg gac tca aaa ggg cga	1633
Arg Lys Arg Ser Ser His Leu Ser Ser Ser Ser Asp Ser Lys Gly Arg	
530 535 540	
cca tca ttc taa	1645

Pro Ser Phe
545

<210> 18
<211> 547
<212> PRT
<213> Zea mays

<220>
<221> VARIANT
<222> (0)...(0)
<223> Xaa = any amino acid

<400> 18

Ala	Asp	Gly	Arg	Arg	Tyr	Met	Ile	Arg	Arg	Arg	Leu	Leu	Leu	Thr	Gly
1				5					10					15	
Thr	Pro	Ile	Gln	Asn	Ser	Leu	Gln	Glu	Leu	Trp	Ser	Leu	Leu	Asn	Phe
			20					25					30		
Ile	Leu	Pro	Asn	Ile	Phe	Asn	Ser	Gln	Asn	Phe	Glu	Glu	Trp	Phe	
		35					40				45				
Asn	Ala	Pro	Phe	Ala	Cys	Asp	Val	Ser	Leu	Asn	Asp	Glu	Glu	Gln	Leu
	50					55					60				
Leu	Ile	Ile	His	Arg	Leu	His	Gln	Val	Leu	Arg	Pro	Phe	Leu	Leu	Arg
65					70					75					80
Arg	Lys	Lys	Asp	Glu	Val	Xaa	Lys	Tyr	Leu	Pro	Val	Lys	Thr	Gln	Val
				85					90					95	
Ile	Leu	Lys	Cys	Asp	Met	Ser	Ala	Trp	Gln	Lys	Ala	Tyr	Tyr	Glu	Gln
			100					105					110		
Val	Thr	Ser	Arg	Glu	Lys	Val	Ala	Leu	Gly	Tyr	Gly	Ile	Arg	Lys	Lys
		115					120					125			
Ala	Leu	Gln	Asn	Leu	Ser	Met	Gln	Leu	Arg	Lys	Cys	Cys	Asn	His	Pro
	130					135					140				
Tyr	Leu	Phe	Val	Glu	His	Tyr	Asn	Met	Tyr	Gln	Arg	Glu	Glu	Ile	Val
145					150					155					160
Arg	Ala	Ser	Gly	Lys	Phe	Glu	Leu	Leu	Asp	Arg	Leu	Leu	Pro	Lys	Leu
				165					170					175	
Gln	Arg	Ala	Gly	His	Arg	Val	Leu	Leu	Phe	Ser	Gln	Met	Thr	Lys	Leu
			180					185					190		
Leu	Asp	Val	Leu	Glu	Ile	Tyr	Leu	Gln	Met	Tyr	Asn	Phe	Lys	Tyr	Met
		195					200					205			
Arg	Leu	Asp	Gly	Ser	Thr	Lys	Thr	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Ala
	210					215					220				
Asp	Phe	Asn	Lys	Lys	Asn	Ser	Glu	Tyr	Phe	Met	Phe	Leu	Leu	Ser	Thr
225					230					235					240
Arg	Ala	Gly	Gly	Leu	Gly	Leu	Asn	Leu	Gln	Thr	Ala	Asp	Thr	Val	Ile
				245					250					255	
Ile	Phe	Asp	Ser	Asp	Trp	Asn	Pro	Gln	Met	Asp	Gln	Gln	Ala	Glu	Asp
			260					265					270		
Arg	Ala	His	Arg	Ile	Gly	Gln	Lys	Asn	Glu	Val	Arg	Val	Phe	Val	Leu
		275					280					285			
Val	Ser	Val	Gly	Ser	Ile	Glu	Glu	Glu	Ile	Leu	Asp	Arg	Ala	Lys	Gln
	290					295					300				
Lys	Met	Gly	Ile	Asp	Ala	Lys	Val	Ile	Gln	Ala	Gly	Leu	Phe	Asn	Thr
305					310					315					320
Thr	Ser	Thr	Ala	Gln	Asp	Arg	Arg	Ala	Leu	Leu	Gln	Glu	Ile	Leu	Arg


```

<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (6)...(514)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G; Xaa = Any Amino Acid

<400> 21
ccnta aat ttc ttg tta ccc aaa cnt nat caa ttt cat cca gga gga ctt      50
      Asn Phe Leu Leu Pro Lys Xaa Xaa Gln Phe His Pro Gly Gly Leu
        1             5             10             15

ctc tca aat ggt tta ata agc cat ttg aga gtg ctt gga gat agc tcg      98
Leu Ser Asn Gly Leu Ile Ser His Leu Arg Val Leu Gly Asp Ser Ser
          20             25             30

cct gat gaa gct tta ntg tcc gag gag gag aat ctc ttg att ata aat      146
Pro Asp Glu Ala Leu Xaa Ser Glu Glu Glu Asn Leu Leu Ile Ile Asn
          35             40             45

cgt ctg cac caa gtt ttg aga cca ttt gta ctt agg agg ctg aaa cac      194
Arg Leu His Gln Val Leu Arg Pro Phe Val Leu Arg Arg Leu Lys His
          50             55             60

aag gtt gaa aat gag ttg cct gag aag att gag aga cta ata aga tgt      242
Lys Val Glu Asn Glu Leu Pro Glu Lys Ile Glu Arg Leu Ile Arg Cys
          65             70             75

gag gcc tca tca tat caa aaa ctt ttg atg aag agg gtg gaa gaa aat      290
Glu Ala Ser Ser Tyr Gln Lys Leu Leu Met Lys Arg Val Glu Glu Asn
          80             85             90             95

ctt ggt tct att ggc aat tca aag gct cga tca gta cac aac tct gtc      338
Leu Gly Ser Ile Gly Asn Ser Lys Ala Arg Ser Val His Asn Ser Val
          100            105            110

atg gag ctt cgt aat ata tgc aat cat cca tat ctc agt cag ctt cat      386
Met Glu Leu Arg Asn Ile Cys Asn His Pro Tyr Leu Ser Gln Leu His
          115            120            125

gca gag gag gtg gat aac ttc ata cct aaa cat tat ctg cca cca att      434
Ala Glu Glu Val Asp Asn Phe Ile Pro Lys His Tyr Leu Pro Pro Ile
          130            135            140

att aga ctt tgt ggg aag ctt gag atg ttg gac cgt tta ttg cca aaa      482
Ile Arg Leu Cys Gly Lys Leu Glu Met Leu Asp Arg Leu Leu Pro Lys
          145            150            155

ttg aag gcg aca gat cat cgg gtt ctt ttc tt                          514
Leu Lys Ala Thr Asp His Arg Val Leu Phe
          160            165

```

<210> 22
 <211> 169
 <212> PRT
 <213> Glycine max

<220>
 <221> VARIANT
 <222> (0)...(0)
 <223> Xaa = Any Amino Acid

<400> 22
 Asn Phe Leu Leu Pro Lys Xaa Xaa Gln Phe His Pro Gly Gly Leu Leu
 1 5 10 15
 Ser Asn Gly Leu Ile Ser His Leu Arg Val Leu Gly Asp Ser Ser Pro
 20 25 30
 Asp Glu Ala Leu Xaa Ser Glu Glu Asn Leu Leu Ile Ile Asn Arg
 35 40 45
 Leu His Gln Val Leu Arg Pro Phe Val Leu Arg Arg Leu Lys His Lys
 50 55 60
 Val Glu Asn Glu Leu Pro Glu Lys Ile Glu Arg Leu Ile Arg Cys Glu
 65 70 75 80
 Ala Ser Ser Tyr Gln Lys Leu Leu Met Lys Arg Val Glu Glu Asn Leu
 85 90 95
 Gly Ser Ile Gly Asn Ser Lys Ala Arg Ser Val His Asn Ser Val Met
 100 105 110
 Glu Leu Arg Asn Ile Cys Asn His Pro Tyr Leu Ser Gln Leu His Ala
 115 120 125
 Glu Glu Val Asp Asn Phe Ile Pro Lys His Tyr Leu Pro Pro Ile Ile
 130 135 140
 Arg Leu Cys Gly Lys Leu Glu Met Leu Asp Arg Leu Leu Pro Lys Leu
 145 150 155 160
 Lys Ala Thr Asp His Arg Val Leu Phe
 165

<210> 23
 <211> 23
 <212> DNA
 <213> Glycine max

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 23
 aacccgatga tctgtcgcc tca

23

<210> 24
 <211> 23
 <212> DNA
 <213> Glycine max

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 24
tcatccagga ggactttctct caa 23

<210> 25
<211> 403
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (221)...(403)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G

<400> 25
tgaatatntn cttgntttta atttatgcga ntaaggattt gtgcattnngg agattagtgt 60
cnaatgaatca agtgattgnt attttatttc atgtgtcacc cagccatatt ggcagatgaa 120
atgggtcttg gcaaaacagt tcaggtagct attctgtttt ttattatttt aatatgtttc 180
ntaatttggt tgtnttccta atcctttact tttcaagtaa gaa atg cca tat gtt 235
Glu Met Pro Tyr Val
1 5

ctt gtc ttc cag gcc atc aca tat tta act ttg ctg aaa cac ttg cac 283
Leu Val Phe Gln Ala Ile Thr Tyr Leu Thr Leu Leu Lys His Leu His
10 15 20

aat gat tct ggt cca cat ctt ata gta tgt cct gct tct gtt ctg gaa 331
Asn Asp Ser Gly Pro His Leu Ile Val Cys Pro Ala Ser Val Leu Glu
25 30 35

aac tgg gaa agg gaa tta aaa agg tgg tgt cca tcc ttt tct gtt ctt 379
Asn Trp Glu Arg Glu Leu Lys Arg Trp Cys Pro Ser Phe Ser Val Leu
40 45 50

caa tac cat ggg gcc gga cgt gca 403
Gln Tyr His Gly Ala Gly Arg Ala
55 60

<210> 26
<211> 61
<212> PRT
<213> Glycine max

<220>
<221> VARIANT
<222> (0)...(0)
<223> Xaa = Any Amino Acid

<400> 26
Glu Met Pro Tyr Val Leu Val Phe Gln Ala Ile Thr Tyr Leu Thr Leu
1 5 10 15
Leu Lys His Leu His Asn Asp Ser Gly Pro His Leu Ile Val Cys Pro
20 25 30

Ala	Ser	Val	Leu	Glu	Asn	Trp	Glu	Arg	Glu	Leu	Lys	Arg	Trp	Cys	Pro
		35					40					45			
Ser	Phe	Ser	Val	Leu	Gln	Tyr	His	Gly	Ala	Gly	Arg	Ala			
	50					55					60				

<210> 27
 <211> 23
 <212> DNA
 <213> Glycine max

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 27
 gccccatggt attgaagaac aga 23

<210> 28
 <211> 25
 <212> DNA
 <213> Glycine max

<220>
 <221> primer_bind
 <222> (1)...(25)

<400> 28
 attttatttc atgtgtcacc cagcc 25

<210> 29
 <211> 522
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (1)...(522)

<221> misc_feature
 <222> (0)...(0)
 <223> n = A, T, C or G; Xaa = Any Amino Acid

<400> 29
 gtt tct ggg agg aag gct cag tat tct aag aaa aac tca cgt aat gta 48
 Val Ser Gly Arg Lys Ala Gln Tyr Ser Lys Lys Asn Ser Arg Asn Val
 1 5 10 15

gat tca ctc cct ttg atg gag ggt gaa ggg cgt gct tta aaa gtt tat 96
 Asp Ser Leu Pro Leu Met Glu Gly Glu Gly Arg Ala Leu Lys Val Tyr
 20 25 30

gga ttc aat cac gtt caa cga aca caa ttc cta cag aca ctc atg agg 144
 Gly Phe Asn His Val Gln Arg Thr Gln Phe Leu Gln Thr Leu Met Arg
 35 40 45

tat ggt ttt cag aac tat gat tgg aaa gag tat ctt cct cgt ttg aag 192

Tyr	Gly	Phe	Gln	Asn	Tyr	Asp	Trp	Lys	Glu	Tyr	Leu	Pro	Arg	Leu	Lys		
	50					55					60						
ggg	aaa	agt	gtt	gag	gaa	att	cag	aga	tat	ggt	gag	ctt	gtc	atg	gcc	240	
Gly	Lys	Ser	Val	Glu	Glu	Ile	Gln	Arg	Tyr	Gly	Glu	Leu	Val	Met	Ala		
	65				70				75					80			
cat	ctt	gta	gag	gac	aca	aat	gac	tca	cca	acc	tat	gca	gat	ggt	gtg	288	
His	Leu	Val	Glu	Asp	Thr	Asn	Asp	Ser	Pro	Thr	Tyr	Ala	Asp	Gly	Val		
				85				90						95			
ccg	aag	aaa	tgc	gtg	ctg	atg	aga	cat	tgg	tca	ggc	tag	cca	aaa	tat	336	
Pro	Lys	Lys	Cys	Val	Leu	Met	Arg	His	Trp	Ser	Gly	*	Pro	Lys	Tyr		
			100					105						110			
cac	ttg	tgg	agg	aga	agg	tgg	tgc	atg	gag	caa	gga	aaa	tta	caa	aac	384	
His	Leu	Trp	Arg	Arg	Arg	Trp	Cys	Met	Glu	Gln	Gly	Lys	Leu	Gln	Asn		
			115					120					125				
tct	tcc	cca	act	act	tga	tgt	atg	aat	tta	ctg	gct	tat	cag	gtg	gaa	432	
Ser	Ser	Pro	Thr	Thr	*	Cys	Met	Asn	Leu	Leu	Ala	Tyr	Gln	Val	Glu		
		130						135					140				
gaa	tat	gga	aag	ggg	aac	atg	atc	tac	tgt	nac	tga	agc	ata	ata	agc	480	
Glu	Tyr	Gly	Lys	Gly	Asn	Met	Ile	Tyr	Cys	Xaa	*	Ser	Ile	Ile	Ser		
		145					150						155				
acg	ggt	tgc	cag	tgg	cat	aca	tat	cag	atn	cag	aga	tac	ggg			522	
Thr	Gly	Cys	Gln	Trp	His	Thr	Tyr	Gln	Xaa	Gln	Arg	Tyr	Gly				
		160					165					170					

<210> 30
 <211> 171
 <212> PRT
 <213> Oryza sativa

<220>
 <221> VARIANT
 <222> (0)...(0)
 <223> Xaa = Any Amino Acid

<400> 30																	
Val	Ser	Gly	Arg	Lys	Ala	Gln	Tyr	Ser	Lys	Lys	Asn	Ser	Arg	Asn	Val		
1				5					10					15			
Asp	Ser	Leu	Pro	Leu	Met	Glu	Gly	Glu	Gly	Arg	Ala	Leu	Lys	Val	Tyr		
			20					25					30				
Gly	Phe	Asn	His	Val	Gln	Arg	Thr	Gln	Phe	Leu	Gln	Thr	Leu	Met	Arg		
		35				40					45						
Tyr	Gly	Phe	Gln	Asn	Tyr	Asp	Trp	Lys	Glu	Tyr	Leu	Pro	Arg	Leu	Lys		
	50				55					60							
Gly	Lys	Ser	Val	Glu	Glu	Ile	Gln	Arg	Tyr	Gly	Glu	Leu	Val	Met	Ala		
65				70					75					80			
His	Leu	Val	Glu	Asp	Thr	Asn	Asp	Ser	Pro	Thr	Tyr	Ala	Asp	Gly	Val		
			85					90						95			
Pro	Lys	Lys	Cys	Val	Leu	Met	Arg	His	Trp	Ser	Gly	Pro	Lys	Tyr	His		

				100				105					110		
Leu	Trp	Arg	Arg	Arg	Trp	Cys	Met	Glu	Gln	Gly	Lys	Leu	Gln	Asn	Ser
		115					120					125			
Ser	Pro	Thr	Thr	Cys	Met	Asn	Leu	Leu	Ala	Tyr	Gln	Val	Glu	Glu	Tyr
	130					135					140				
Gly	Lys	Gly	Asn	Met	Ile	Tyr	Cys	Xaa	Ser	Ile	Ile	Ser	Thr	Gly	Cys
145					150					155					160
Gln	Trp	His	Thr	Tyr	Gln	Xaa	Gln	Arg	Tyr	Gly					
				165				170							

aaa agg aaa cgg agc aag cta aca gtt agt cca tca agt gag cat gat	193
Lys Arg Lys Arg Ser Lys Leu Thr Val Ser Pro Ser Ser Glu His Asp	
50 55 60	
gct tcc tca cca ata ctg gat tct caa atg aac aat ggc tcc atc aaa	241
Ala Ser Ser Pro Ile Leu Asp Ser Gln Met Asn Asn Gly Ser Ile Lys	
65 70 75 80	
aag aag atc aaa cat gac act aac att tct cca tca acc aag aag ata	289
Lys Lys Ile Lys His Asp Thr Asn Ile Ser Pro Ser Thr Lys Lys Ile	
85 90 95	
aga gga cat gac ggg tac ttc tac gag tgt gta gaa tgt gat ctc ggt	337
Arg Gly His Asp Gly Tyr Phe Tyr Glu Cys Val Glu Cys Asp Leu Gly	
100 105 110	
ggc aat ttg ctg tgc tgt gat agc tgt cca cga aca tac cac ttg gaa	385
Gly Asn Leu Leu Cys Cys Asp Ser Cys Pro Arg Thr Tyr His Leu Glu	
115 120 125	
tgt ctt aat cct cct ctc aag cgt gca cca cct gga aat tgg caa tgc	433
Cys Leu Asn Pro Pro Leu Lys Arg Ala Pro Pro Gly Asn Trp Gln Cys	
130 135 140	
cca aga tgt cgt aca aaa aaa gtt agc ttg aag ctc tta aac aat gct	481
Pro Arg Cys Arg Thr Lys Lys Val Ser Leu Lys Leu Leu Asn Asn Ala	
145 150 155 160	
gat gct gac acc tcc taa acg tga aag aa	510
Asp Ala Asp Thr Ser * Thr * Lys	
165	

<210> 34

<211> 167

<212> PRT

<213> Oryza sativa

<400> 34

Leu Gln Asp Phe Gly Gly Gly Gly Cys Gly Cys Leu Glu Arg Arg Gly	
1 5 10 15	
Leu Ile Ala Thr Ala Cys Asp Val Asp Thr Leu Met Met Lys Glu Arg	
20 25 30	
Ser Ser Leu Cys Glu Ser Ala Ala Asp Gly Ser Trp Val Leu Lys Tyr	
35 40 45	
Lys Arg Lys Arg Ser Lys Leu Thr Val Ser Pro Ser Ser Glu His Asp	
50 55 60	
Ala Ser Ser Pro Ile Leu Asp Ser Gln Met Asn Asn Gly Ser Ile Lys	
65 70 75 80	
Lys Lys Ile Lys His Asp Thr Asn Ile Ser Pro Ser Thr Lys Lys Ile	
85 90 95	
Arg Gly His Asp Gly Tyr Phe Tyr Glu Cys Val Glu Cys Asp Leu Gly	
100 105 110	
Gly Asn Leu Leu Cys Cys Asp Ser Cys Pro Arg Thr Tyr His Leu Glu	
115 120 125	
Cys Leu Asn Pro Pro Leu Lys Arg Ala Pro Pro Gly Asn Trp Gln Cys	

130		135		140
Pro Arg Cys Arg Thr Lys Lys Val Ser Leu Lys Leu Leu Asn Asn Ala				
145		150		155
Asp Ala Asp Thr Ser Thr Lys				160
		165		

<210> 35
 <211> 23
 <212> DNA
 <213> Oryza sativa

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 35
 cttacaggat ttcgggggag gtg 23

<210> 36
 <211> 23
 <212> DNA
 <213> Oryza sativa

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 36
 ctttcacggt taggaggtgt cag 23

<210> 37
 <211> 667
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (2)...(667)

<221> misc_feature
 <222> (0)...(0)
 <223> n = A, T, C, or G; Xaa = Any Amino Acid

<400> 37
 g ttg act gga acc cca tta cag aac aac att ggt gaa atg tat aat ttg 49
 Leu Thr Gly Thr Pro Leu Gln Asn Asn Ile Gly Glu Met Tyr Asn Leu
 1 5 10 15

ttg aac ttc cta cag cct gct tct ttc cct tct cta gca tca ttt gag 97
 Leu Asn Phe Leu Gln Pro Ala Ser Phe Pro Ser Leu Ala Ser Phe Glu
 20 25 30

gag aag ttt aat gaa ctt gca aca gca gag aaa gtg gag gag ctg aag 145
 Glu Lys Phe Asn Glu Leu Ala Thr Ala Glu Lys Val Glu Glu Leu Lys
 35 40 45

aaa ctg gta gca cca cat atg ctt cga agg ctg aaa aaa gat gca atg Lys Leu Val Ala Pro His Met Leu Arg Arg Leu Lys Lys Asp Ala Met 50 55 60	193
aaa aat atc ccc ccg aag aca gag cga atg gtg cct gtc gaa ctg aca Lys Asn Ile Pro Pro Lys Thr Glu Arg Met Val Pro Val Glu Leu Thr 65 70 75 80	241
tca atc cag gct gaa tac tac cgt gct atg ctt aca aag aac tac caa Ser Ile Gln Ala Glu Tyr Tyr Arg Ala Met Leu Thr Lys Asn Tyr Gln 85 90 95	289
gta ctg cgt aat acc gga aaa ggt ggt gct cat cag tca ttg ctc aat Val Leu Arg Asn Thr Gly Lys Gly Gly Ala His Gln Ser Leu Leu Asn 100 105 110	337
ata gta atg cag ctt cgg aaa ttt gca acc atc cat atc tta tcc tgg Ile Val Met Gln Leu Arg Lys Phe Ala Thr Ile His Ile Leu Ser Trp 115 120 125	385
gaa ctg aac ccg aat caa gtt cac cag att ttt gca tga aat gag aat Glu Leu Asn Pro Asn Gln Val His Gln Ile Phe Ala * Asn Glu Asn 130 135 140	433
aaa ggc tca aca aat taa ctt tgt tgc att cta tgc tca aag tgt tac Lys Gly Ser Thr Asn * Leu Cys Cys Ile Leu Cys Ser Lys Cys Tyr 145 150 155	481
aca gtg atg ggc atc gtg ttc taa ttt tcc aga tga cta aac tct tga Thr Val Met Gly Ile Val Phe * Phe Ser Arg * Leu Asn Ser * 160 165 170	529
cat ccc gaa gat anc gac ccg gaa ttg gca taa aca ntn aaa gag naa His Pro Glu Asp Xaa Asp Pro Glu Leu Ala * Thr Xaa Lys Glu Xaa 175 180 185	577
tgg tcg tgt cgt ggg tga cnc aag cac ata nct tca aca gaa ana cgt Trp Ser Cys Arg Gly * Xaa Lys His Ile Xaa Ser Thr Glu Xaa Arg 190 195 200	625
ttg att tgt aca acg gca tgc ntg tat tga cna nac gta can Leu Ile Cys Thr Thr Ala Cys Xaa Tyr * Xaa Xaa Val Xaa 205 210	667

<210> 38

<211> 214

<212> PRT

<213> Triticum aestivum

<220>

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Any Amino Acid

<400> 38

Leu Thr Gly Thr Pro Leu Gln Asn Asn Ile Gly Glu Met Tyr Asn Leu
 1 5 10 15
 Leu Asn Phe Leu Gln Pro Ala Ser Phe Pro Ser Leu Ala Ser Phe Glu
 20 25 30
 Glu Lys Phe Asn Glu Leu Ala Thr Ala Glu Lys Val Glu Glu Leu Lys
 35 40 45
 Lys Leu Val Ala Pro His Met Leu Arg Arg Leu Lys Lys Asp Ala Met
 50 55 60
 Lys Asn Ile Pro Pro Lys Thr Glu Arg Met Val Pro Val Glu Leu Thr
 65 70 75 80
 Ser Ile Gln Ala Glu Tyr Tyr Arg Ala Met Leu Thr Lys Asn Tyr Gln
 85 90 95
 Val Leu Arg Asn Thr Gly Lys Gly Gly Ala His Gln Ser Leu Leu Asn
 100 105 110
 Ile Val Met Gln Leu Arg Lys Phe Ala Thr Ile His Ile Leu Ser Trp
 115 120 125
 Glu Leu Asn Pro Asn Gln Val His Gln Ile Phe Ala Asn Glu Asn Lys
 130 135 140
 Gly Ser Thr Asn Leu Cys Cys Ile Leu Cys Ser Lys Cys Tyr Thr Val
 145 150 155 160
 Met Gly Ile Val Phe Phe Ser Arg Leu Asn Ser His Pro Glu Asp Xaa
 165 170 175
 Asp Pro Glu Leu Ala Thr Xaa Lys Glu Xaa Trp Ser Cys Arg Gly Xaa
 180 185 190
 Lys His Ile Xaa Ser Thr Glu Xaa Arg Leu Ile Cys Thr Thr Ala Cys
 195 200 205
 Xaa Tyr Xaa Xaa Val Xaa
 210

<210> 39
 <211> 23
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 39
 gttgactgga accccattac aga

23

<210> 40
 <211> 23
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 40
 catgccgttg tacaaatcaa acg

23

<210> 41
 <211> 12561
 <212> DNA

<213> Zea mays

<220>

<221> misc_feature

<222> (1)...(12561)

<223> Zmpk1 genomic sequence

<221> misc_feature

<222> (0)...(0)

<223> n = A, T, C, or G

<400> 41

atactgtaat	catctatgac	aggtgaaaaa	tctctctgtt	tagacaaaac	agttaacata	60
atggattcgc	ttcaatttct	cacctatgta	tgtacagtga	ttggaaccca	catgcggatt	120
tgcaagctat	ggcaagagct	catcgcttag	gacagactag	taaggatatt	taccttacac	180
tttatattgt	ataaaaaaac	agattttcaa	taagttttgt	ggtgatttta	taattttcat	240
ctgtttttct	tttaggtgat	gatatacagg	cttgtaggcc	gaggtacaat	tgaggagcga	300
atgatgcagc	ttacaaaaaa	gaagatttta	ttggagcact	tagttgttgg	tcgactcacc	360
aaagctaata	atgtcaatca	ggtatgttga	ctacttttta	atggtgaatt	ttgtaaacca	420
tcaacttagg	ttgatctttt	atggcctaag	ctatttatga	attcatttat	ggattgaggg	480
ttgagtagtt	acatgttact	ccctccattt	tttatatttg	tgggtgttta	gttcaaaaat	540
aaactaacgg	gtgacaaata	ttcgagaacg	gaggtagtac	tagtaccttc	tgtctgggat	600
gacatgaaat	gaatgtagca	tctgttagta	tcatgtccat	ttctttgtgt	tacattttac	660
aaggcttaaa	accttacaca	tattgccgga	gttggtgact	atttagtctt	atctgtaaatt	720
ttagttgttt	ctcttgatgt	caatagcaat	ttatggttgt	atgagatttc	gtgggtttgt	780
tagcatgtgt	gccatatagg	tttagctccg	ctgatgtgtt	atgcacttat	aattcagacc	840
cattttggag	ctgtgatgtg	atacacaatg	ctagttgtta	aggccccatt	tgtttgtttc	900
atattcataa	tctatgtgca	tgcattagtc	cagatcaggc	tgggtgatct	ggtgggcatt	960
ggtacatgca	tggctgaata	agagtttgat	gaccaagggg	aaggcacccc	acatctactc	1020
ttggctggcc	aactgggtag	tatctgctag	ttatcatgga	aataagggtg	gcaacctctt	1080
taaggttgtc	ttcaagaact	aaacataaaa	agaatgccat	gaagatggaa	cccaggatct	1140
caggacctat	ttgtcgtaa	atcttctgaat	ctttgctgga	gctggcaacg	ggctggttgc	1200
tggctctcatc	cctacattat	agttttgtgt	atgtttcttc	cagactttca	acacttctca	1260
acttctagaa	catgtaaccg	gcatgtacaa	acagaacaat	ttagaacagt	tcaaagtgca	1320
tgtccttact	gcgatgggac	cacacacttc	tggctctctt	aggacttgat	tgatttaattg	1380
cagattaact	attaacccaa	tttgtctctc	tgacctgcta	gtgagccctt	cattggtttt	1440
taagctactaa	ataataaata	tgtgtctttg	cctattttag	gaggagtgtg	atgatattat	1500
acgctatgga	tcaaaggagc	tttttgaaga	cgagaatgat	gaatctcgcc	aaattcatta	1560
tgacgaagct	gcaattgaga	ggtaaacacc	taggcccttt	tttgatctcc	taagataaga	1620
ttaatgagaa	cgacgtagaa	aaatgagtgt	gatccaagca	cagattctag	aatccaacta	1680
tctagctaaa	ccttgctata	catagattct	cgctatgcaa	aggccataat	cactatgaaa	1740
atgagatcca	aacacccctt	gttttttatt	atctagaatg	tagattctca	aaagaagggc	1800
aagcttggtg	cattggtgag	atctttctca	ttcagtcatc	aagtcgtggg	ttcaaagcag	1860
cctctcgaca	tttgtgggag	cctctagcac	tgggtctacc	cctttttatt	aacaatctag	1920
attctacatc	atcatgtaga	atcactatga	taatgagatc	taaacatggc	cttaagcccc	1980
taacttcacc	ttgggaagtt	atttcgtgca	ttaagcatgc	ctttttgggtg	tgaagttgtt	2040
taaagtatta	ccagatttat	gtaacaattt	acaaatgtat	tggaaatctgg	agaccatttt	2100
gatcatggat	gcaaatctag	aattctagag	ataattagta	tgtatgccct	accaagtagg	2160
atacgatgag	agattgagag	tgctaagaga	cttttatggg	aagacttaga	tggtatgatt	2220
agagttatgc	ctattagtga	gaagcttttc	ataggagatc	tcaacggaca	tgtaggtaca	2280
acaagtgtag	gtttcaaggc	ggttcattgga	gggtttgagg	aagagaatcc	cattttgtga	2340
catgtagtag	tggaacacgc	tctagtcaga	tttgtaaagt	aactgtgtat	tccttgtaat	2400
gggatcttgc	gtaatgagca	taggccctat	aactctatta	taaatacagc	accgaaccct	2460
gatgttaagc	taggttttagc	ctcctctctc	ccacctagcc	aatatgggtat	caagctaggt	2520
ttagcctcct	ctctcccacc	cagccgtcgc	cgccaccgct	acagtagttg	ccgctgtcgg	2580
cattcttcct	cccctcccc	ttccctggtg	tcggcgaccc	tccttcgacc	tccttcctac	2640

ggcgccccctt	tccccctcgtc	cagccgctcgc	cgcagtgctct	ggacgcgagg	cccttcctca	2700
tccgtgcgct	tggggggccgc	tgggcttttc	ctccccccgc	ccgccagcag	tcggccttgt	2760
cctcgccacc	gtcggagttg	ccacatgaga	ggcattgaaa	gggtgaaagg	aggtaatgcg	2820
gtgggcccctg	atgttatccc	aatcgaggca	tggagatgtc	ttggggggaca	tagctataat	2880
aggctaacta	agttgttcag	tctatcttcc	ggtcaaacaa	gatgcttgac	aagtggagaa	2940
gtatatgttg	accaatcgac	aaaaataaag	aagatattca	aagttgtagc	aattaatagg	3000
gaataaagtt	gatgagccat	actacgaagc	tatgggagag	agttatcgag	catcgagagg	3060
aaaaacgagg	acctgtatga	accaattttg	tttcatgcaa	gctcaaccat	ggaagccatt	3120
ttcttaataa	gataagtact	ttgtgactaa	cataaaattt	tatgtggtag	gctttggaca	3180
aacataaaat	tccaacgaag	tactttgtga	ctaattaagg	acatgtacaa	taatggtgtg	3240
actagtcaact	agtgtttgaa	caagtcatgt	gaacacaaat	gacttactga	ttagagtagg	3300
gctacatcag	gggtcaacct	tgagctctta	cctttttgcc	ttggtgatgg	atgaggtcac	3360
aaaggacata	caaatggata	tcccttggtt	tatgccttgc	ggacgatata	gcgttattttg	3420
atgaaagtcg	gatagagtta	tttgatggaa	gtcggatagg	agtaaatagg	aaactatagc	3480
tgtggcggga	gactctagag	tccaaagggt	ttagactcaa	tagaaactaaa	actgaataca	3540
tgagatgtgt	cttcggcact	actacacata	aggaaaacga	tgttagtttg	aaaggtcaag	3600
tagtgccctac	gaaacgataa	tatacatgat	agattagggg	tgacaccaat	tgaagaaaag	3660
cttttccaac	accgattgat	atggtttgaa	catgtctaac	agagacctct	agagacacca	3720
atgtgtagtg	gaattctaag	tcatgatagt	aatgagaaga	gacaagagag	gcagaggaag	3780
gccaaagtgtg	acatggaaat	gggtagtaga	agagatttca	aaggatgaaa	tataccaaag	3840
atthagcctt	aaataggagc	gaatgggaaa	caactcatcc	atgtgcctga	atcttgattt	3900
gtggctttat	taggtttcaa	ctctagccta	gcccaacttg	attgggacta	ataggctttg	3960
ttgttgtttt	tgcaaacctg	gaaattttca	tgaccatggc	aataaatagc	acagtttata	4020
ctcaatatca	ccctatacgt	aagaacaaca	tgagctgcat	aattgatttt	gtttgtttta	4080
ttccattttc	ttatgaaatt	ccttcttttc	tcctattaca	gtaattcata	gtatggaatc	4140
tgtcttcatg	cagattatgc	acaacactaa	tccttggtgt	tatggcccca	atttttatct	4200
tctttgttat	gacttaaaac	tgtagtgtct	tatgttagag	gagacaacgt	aataatctctg	4260
actggactca	caggttggtta	gaccgtgatc	aagttgacgg	tgatgaatct	gtggaagatg	4320
aagaagaaga	tggttcttta	aaaggattca	aggtattggg	gtcttctttc	aattattaca	4380
agcataatgc	ttgaggagct	tcttcatttt	aattatcctc	ttgatattta	ctgtggttta	4440
cattgttttag	tctttttctt	gtttattatg	tgacatgta	tttgttaaag	tgacataat	4500
ctctatttgc	acaagtacac	ttgtgaggca	gtgaggtctg	actctgttat	ttgtatgttt	4560
gcgagtatgc	atgtaatcaa	gccactattg	atatttgata	ggattaacct	atgcatcaga	4620
ttttgttgat	gaatgagata	ttttatgtat	gcattgcatg	ctttctcatt	tgaattatct	4680
cgttagtttt	acctgcccac	ctaagatata	caattgcgta	gtgctgagta	aaacactatg	4740
caaataaaca	atgtttcttg	ttctctcatt	catctgtagg	cctattcttc	caattcaaac	4800
atgctatgtt	actcataggg	caatactatt	tgtgtttcat	ttattgttga	aaatgctgca	4860
tactacaact	gcctcatgac	tcattttttca	ttctaagtgt	ttggcacatt	ctagcacaac	4920
aaagagtccc	tttatttaac	ccaaagcaaa	acgattctcg	cttcttgtat	tactctatgc	4980
taggttgcaa	actttgaata	tatcgatgag	gcaaaggctc	aggcagaaaa	agaggaggca	5040
cggagaaagg	ctgcagctga	ggctgaaaat	tctgaaaaga	actactggga	tgaactattg	5100
aaggatagat	atgatgtaca	gaaagttgaa	gaacatactg	ctatgggaaa	agggaaaaga	5160
agccgcaaac	aggtttaatt	tctaaccatt	tccattgtta	accttgtgac	ttgtgcccct	5220
tttcatatca	ttttcccttg	ttttgtgatc	tgcatctcatt	gctttgcggt	tggcaataga	5280
tgtaatttca	tatttgttcc	ttcccaaaaa	gaaaatcata	gttgttgcct	tgttggcaac	5340
ttacagtatt	tcacttgtag	aatatctttt	aaactcgatt	taagcactgt	aattgtaatt	5400
aaatttttagg	aaatcatgct	tatacaccaa	ctaggataac	tgatgcaacc	aatcactgtt	5460
gagcgttgac	aatatgcatc	aaagtcatat	aactaatctt	atcatgaaga	taagcatgaa	5520
attaaggaag	aacgtagcca	ttatttggtta	tatctttctt	ggtttaacgg	cgcagtgcca	5580
ttagtgcat	acttcttagc	cagacatgac	atctgctgct	cagtgtagt	taatcttctt	5640
ttgcgaagg	acttctcttt	aaactagttt	tgcatgacga	tgaagttgag	tatagacatt	5700
ttgtgttaga	tccttcttgc	tgttactgta	cagtatatat	attagttcat	tattcgtccc	5760
acccaccccc	aaaccaatca	ttgactatag	cttaatgtac	tatgtctgtt	tggtaatgta	5820
ttgtattgtt	tttatttggg	cgattttaa	tttagagtga	ccatatacat	tttcagtaag	5880
agaaaagact	gatgaacctt	gtttcttttc	tgcgctcatgt	gcagatggct	gccgctgatg	5940
aagatgacat	tcatgattta	agttccgaag	atgaggatta	ctcattggag	gatgacattt	6000

cagataatga	cacaagtttg	caaggaaata	tttctgggaa	gaggggcca	tattctaaga	6060
gaaaatcacg	taagagagca	atgtaaatac	atcgactat	ggactattgt	tacatgatga	6120
atattctgta	cttatatact	ttgcaaatac	attgtcatta	ggtaatgttg	attctattcc	6180
attgatggag	ggcgaaggac	gtaccttgag	agttcttgga	ttcaaccatg	ctcaacgagc	6240
aatgttccta	cagacactca	ataggttagt	tactgatatg	cctcttgaac	ctgtctggtc	6300
agcgagtga	taccttgaac	ctaaagttta	tgtgcagatg	ttgagatgct	attacattgc	6360
gtgataaagc	aggcacacag	aaatttctgt	ttcatttgta	tctcttggcc	atgtgtacat	6420
ttttaatcat	ggaatccttt	tttttttaca	attgttgggt	agtgtttaca	tttttatcac	6480
tcgtttctaa	tagttgtgtg	ctctgacctg	tatctttgtc	accaaattgt	aatttctggg	6540
ccaattttaa	gcataaaata	tttgactga	ggtcattggc	tattccctag	ttgtactatc	6600
agaccaacat	gaacgtgacc	ccatgcaaca	ttgtagattc	ggttttcaga	attatgactg	6660
gaaagagtat	cttcctcgtc	ttaaaggaaa	aagtgtcgag	gaaatccaga	ggtatgtgaa	6720
atgtgctctc	catgttttat	gaccccaatt	attttgagtt	gtagaccaaa	tagtgaagaa	6780
tctggggcat	agtttcgtaa	gttagatgga	tatgatgcac	aacattttac	attttattga	6840
ttttctctta	ggcgaagggc	gggcctgggt	cagcggtaga	gcctaccgtc	tgtaacggga	6900
aggtccttgg	ttcgagcccc	aacctctgca	tattatgcgg	gtaaggcttg	gcgcttaaag	6960
atacccttcc	ccagaccccc	cacagtgcga	gaagcctatg	gactgggtt	cgccctttta	7020
ttgattttct	cttaggcccc	gtttgtttcc	cttcatttta	aggaattgga	atctaactga	7080
tggagtaagc	tatttttttt	ataatgtaat	attccataac	tttccaaagt	ttaggtataa	7140
gccaatctca	aattcatggg	gtgagagatg	gaaattgatt	ctatagattt	acatgtact	7200
tttcaaattt	acaacttata	gcacactctt	ctacttgctt	ctctatatga	taaatgtagt	7260
gtataactat	ctctcttata	tgatttagga	taatatacaa	atacattaca	tagataaata	7320
tattaactta	atagttttat	cttaaattat	aattattata	atggaattca	attccaacga	7380
aacaaaacgg	gccttaggta	tatagacaat	gaattcaagt	ttgtgcttcg	acgaagaatt	7440
gatgagatgg	gtaactgggc	attcctggct	tctgatagta	cacatattta	ggcaaagtcg	7500
actgctggta	gtagtgaag	tgtacacaca	aatatgcttg	gttggaactc	tgctttgttt	7560
attatgttgc	aaatttatat	aactattgca	cccttgccaa	caaggaaaga	tgtggcatca	7620
tcacatatga	agccaaatta	agcaggcagt	caccaaagtc	agactataat	tgcatgtcta	7680
gactgttagt	agcaaattga	gccaacagtc	accaaagcta	gactacctct	gaagtgcgaa	7740
tagcaggcgg	ccataaccta	accctattaa	gttgatgca	ccaaccagtt	caacccaaaa	7800
gcttaagctg	atggagagag	gtggcaattc	acttgatttc	taacattctc	cctcacatcg	7860
aggctctctt	agaccgtctc	cagcagttca	cccatacggg	tatcaaaaca	ctggttttca	7920
ctgtagacta	tactgtttgc	atatggggat	gtggatgagt	aagctgctgg	agatagcctt	7980
aggtcttaga	cgtggaataa	gaacggacaa	caattatttt	atttaattgc	gctaaccagg	8040
attcgaactc	aagatatctg	gctttgatat	catattaagt	cgcatatacc	agccagttca	8100
acccaaaaac	ttaagcttat	agagaggtgg	acaattcact	tgtattctaa	caaacccag	8160
tgtagttagc	aaaatgagcc	aacagttacc	aaagcttgca	gctgaagggc	tagtttgga	8220
gcgctttgtg	gacagagcgc	tgcgcgctg	ccaaacactg	ttgctccatc	tcggaagtgc	8280
tcgccctatg	ctccagtcga	tttgcatatt	gggtggggag	cggaaaaaat	ccgctctgtc	8340
tgcagcatgc	tcctctctcc	acttcccgtc	ctgctgcctg	ctccctctc	cacccacgcc	8400
gctatccacc	gcatctctgc	ctgcacagcc	cctctctggc	tcattaacgg	tggcgtggac	8460
cacgagcact	gggcagatcc	gtggtggtga	taaagagggc	aggagggagg	ccagaccctc	8520
cgtggcgagg	agtgtgcac	ttggaggatg	tgggccctgg	cgagctggag	ccgaagctga	8580
tggagaagca	ctaccaaaaca	ctggtatcgg	caggtgggga	gcaacctgag	cgggagccta	8640
ggggagctgg	agccgctggg	agcttcgtga	cagtagtacc	aaacatgatc	taagtaaacg	8700
tcatatgaac	atggaacagg	catcaagatg	ctgtccttca	tatagctcta	tcattacttt	8760
ttccttgtag	agcccataac	cacaagaatg	ttgtacaccc	acttatgtat	agggtaggct	8820
tgtataaacac	ccattttaagt	caagtacacc	tcttatattc	ccaccaaaca	acccagtttt	8880
aggcaattat	ttttgtggag	atcctcaaag	tgattcatag	caataacctt	tgtgcaattt	8940
attttcgtat	atataatatg	ttcttgcaga	tatgctgaac	ttgtcatggc	acatcttgtt	9000
gaagaaatta	atgattctga	ctatttttca	ggtaattgag	cttagtaatg	gctactatca	9060
tttttacgca	tccaattctt	atcctccata	tgcataaatg	cagatggcgt	tccaaaggaa	9120
atgatgcgtg	ttgatgatgt	actagtcagg	atagcaaaca	tatcccttat	tgaggagaag	9180
gtgcatgtgg	ctttcatttg	ttatttgcac	cttaacatga	cttagaactc	aaaagaaact	9240
tatgagcatc	ctgatgatgt	tcaatacaaa	catgattgtg	ctgtattctt	tcttgcgtaa	9300
agtgaagga	ttgtcgagag	ctgaagttta	gtatttaaac	ttgcacctta	tagaattcgg	9360

ttgattacaa	taccttgata	tgattctgct	atcaatgagg	caacctttgt	gtactgtatt	9420
ctttcttact	tttgtattgt	ggttccagat	ggctgccaca	ggaccaggaa	aaattacaaa	9480
catttttcct	aattacttgc	tctatgagtt	ccaaggctta	tctggtggaa	gaatatggaa	9540
agcggagcat	gatctactgt	tactgagagg	catactgaag	tacgaaacta	cgaatatttt	9600
ctttgttaca	atcagctcta	caaaattacc	cctccatgaa	actagcagtg	gctggaacag	9660
ttctggcaag	agtagcctta	aaaagtcgat	gtttgtgtca	gcagcagtg	cgttgcaatg	9720
acagaactga	attgtttggc	tcacttggtg	gttgatggat	tattagtttt	ttagtatagc	9780
agcagtggct	tgcatcttgg	cccagagtga	cctattgtgc	tcagaagtta	gggttaccct	9840
aacgggtatc	ttttcgcata	gcttgatagc	ttccaggtgg	tgctgtcca	cccagtgctc	9900
tagtgatttt	ggagacatcg	ggttcaggaa	ctgtttaatt	aaggcaacaa	attcaactta	9960
tcttaacggt	gagtaagcaa	actgaagtat	cacatgcaaa	ccagatgagc	tccacatttg	10020
atgtgatata	taacttaaat	tatttatatt	gattctgttt	aatactttta	caattgtaat	10080
catgtggaac	agcttaatat	aaaatgtagg	ttttcaagg	gtacacttga	cctgcacagc	10140
gatctccttt	gcttttatag	actttgtgtt	ttttccttgt	ggataatgca	ttttttacca	10200
actattgttt	cacactgtaa	caaaactata	tttaaggtat	taacacaatg	catttgtttt	10260
gccttcacca	ggcatggata	tgcaaggtgg	cagtatatat	cagatgacag	agagaatggg	10320
ctttttgagg	ctgcacgacg	agagcttcat	ctcccttcgg	ttaatgaaat	aattgggtgct	10380
cagttgaacg	aggcaaatgt	tagcatgtgc	tcactatgtc	ccttcctcca	aattttgaag	10440
tgttgcatct	cttatttcct	ccattccttt	tctaggggaa	tttggaaggt	gcacaggaa	10500
gccaagcgaa	cacaacaagc	atgtcgcat	acaaggagac	ccagagaaa	atagttgagt	10560
tcttgagaaa	gagatatcat	cttatggaga	gagccttgaa	tatggaatat	gctgtggtac	10620
ggtagtaggc	ttttttccct	gaacaggcat	gcactcaaag	ctcacatggg	agtgcacagt	10680
agctgttcat	gtagtatctt	gcagcatttt	ttaaagcgta	cctttttctc	ttgcagataa	10740
agaaaaaat	tctgttcct	gatgatatta	ctgaacaagg	tggtccagca	ggacatgctc	10800
cttttattcc	agatatcagt	gaactgttgc	gggaattgcc	caatcttgag	ccaatttgta	10860
agtgatctct	tattccctat	atatatatc	cttctctcca	cctatgcagg	aagagacagt	10920
cacatagtgg	catagaacat	gctggggcag	atgctcacia	tttttaatca	tgtgtcatgc	10980
atgactcttg	tcttactaaa	ctctctctaa	agatgtgttg	ttgttgacat	atactcttga	11040
gtcttgaggt	ttgttcattt	gtttgttttg	ataactggga	tcctcgtttc	cagctaccaa	11100
tgaattgggt	tctgagggca	cagctgggtca	gttacaagtt	ccccatctct	acaataaggt	11160
gtgtaagcgc	aatggcacac	gttttcatgg	gtcatggg	aacgcacat	ttgttttcct	11220
cgagttaaca	ttataaccag	actgtgtacg	tatgctctgc	agatgtgtgg	agtgttgtaa	11280
gagagtgggt	cttatgcgct	cagttccttc	tttgagagaca	agtcgcgcat	ttctagtttg	11340
gccaatagcc	ttcgacaggt	tgaaactgtg	tgcggaatg	tcgtcgaggc	cttgcgacca	11400
caccaaatag	gtactggcag	tgccatcaaa	gaggaattgg	tagatgcagc	caccaaagca	11460
gcagcagcat	gcgctcctca	acaagattca	ggccatgatg	caccgcatgg	gcagctcttc	11520
acagccaagg	cggacatgga	aatcgatgga	tgatttgtag	gttcagagat	ggtaagaaag	11580
ggaatcccc	tctaatacatt	atgtatactg	tggtcagaat	gtgcgctata	tattgtaaca	11640
tcaaagaaag	cacctccagg	cctgaggggtg	ttactgctaa	tgcgtttggt	ttacttggtg	11700
tccttgtaat	atgcatacac	atttagaact	catgcagcca	ttttgtgtgc	tcgaatncgg	11760
tggtatcgct	ccctgttgct	ttgtactgtg	tttaagggcc	tggttggnat	acgaatgggt	11820
aattataaga	cggggctaaa	gataagtacg	gattaactna	tagttggcta	gcttggtggg	11880
taagaaatta	caaaatagtt	tgcaaaaaca	aacatgttgg	tgcaagcgtg	gtcccaaaat	11940
gttaaaaacg	aagaaacgat	ccatgcatat	cttgtaagta	tttacattgg	ctcaattcca	12000
agcaaccttt	gcacttacat	tatacaaaact	agttcaatta	tgcatcttcta	tacttgcttt	12060
ggtttggtgt	ggcatcaatc	accaaaaagg	gggagattga	aagggaatta	ggcttacacc	12120
tatagtccct	aattaatttt	ggtgggtgaa	ttgccaaca	caaataattg	gactaactaa	12180
tttgcccaag	tgtatagaat	atacaggtgt	aaaaggttca	cactcagcca	ataaaaagat	12240
caagttttgg	attcaacaaa	ggagcaaaaga	gacaaccgaa	ggcacctctg	gtctgggggc	12300
accggactgt	ccggtgcacc	agaggactca	aactcaaact	tgccaccttc	gggaattttc	12360
aaaggcactc	cgctataatt	caccggactg	tccggtgtac	accggacagt	gtccggtgct	12420
ccaaggaaga	gcggcctctg	gaactcgcca	gcctcgggaa	aacgcagcgg	ctgctccgct	12480
ataattcacc	ggactgtccg	gtgtacaccg	gactgtccgg	tgaaccagca	gagcaatggc	12540
tacttcacgc	caacggtcac	c				12561

<210> 42
 <211> 4551
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (343)...(4332)

<400> 42

tgccccctct	cctctcctct	cgctcgtgca	gaggaggaga	cagactcccc	ccgtcgccgc	60
cctcgcgcct	cctccgcccc	cagctcaagc	cgagcgtcac	cccgtcggct	accttccatt	120
ctcgcgcgcg	ttctcccact	gggcacctcg	cgccctcgtg	acggtataaa	tagcccctag	180
tactcctcg	gcgctcctca	aaccaccaa	accctagccc	acttagcggc	ggcggcgcta	240
gaggtggaac	gagaccttgg	cggaggtagc	gagggtagcg	ctgctcgtc	gctcgttggg	300
tttccatccc	ctactgccta	gagcgagctc	tacgcgacga	tgagcagcct	tgtcgcgcgg	360
ctgcgcgtgc	ggtcggagag	gcggccgcgg	tacgcgctcg	acgagtccga	cgacgacctc	420
ccgctgcgcg	ttggggccgg	aaaggggaag	gatcaacaga	acgacgcgcc	cgccgagcgg	480
atcgagcgcg	aggacgcgaa	agaagaagct	tgccagcgtc	gtggaaaaag	tgataatcta	540
gtctcttggt	caacatgtac	atacaaat	cacagaaaat	gcttggttcc	ttgcttaaac	600
atcacatctg	ataaatggag	ctgcccagaa	tgtgtaagtc	cattaacata	tatggagagg	660
attctagata	ttgaagtgt	ggaagcacct	cgtgaagatt	ctagttccac	agagcctcga	720
tcaaagaaga	tggagcgata	tcttatcaag	tggaaaggat	tatcatacat	tactgctct	780
tgggtttcag	aaaaagaata	ttcagaagcc	gcgaatatac	accctcgtct	gaggactagg	840
ttgaataact	tcagaaggca	aaaggaagcc	atgaaaatag	aagcagaaaag	atctggtgag	900
gacatcggtg	caattagacc	ggagtggaca	actgttgaca	ggatccttgc	tagcagaaaa	960
aacttagttg	gcgatcggga	atactatgtt	aaatggaatg	aacttacata	tgaggaatgt	1020
acatgggaaa	atgagtctga	catcacggtg	ttccaacctg	agattgaacg	cttcaatgag	1080
atccagttca	ggcgtaaaga	atctggtgac	aagggcaagg	ccactcggga	gccacgccaa	1140
ttcaaggaga	gccctacgtt	tctttctggt	ggcacactac	atccctatca	gcttgaaggg	1200
ttaaactttt	tgcgatattc	gtggtttcat	aacaaacgcg	taatccttgg	tgatgagatg	1260
ggtcttgga	aaacgataca	aagtattgct	tttcttgcc	cactcttga	agacaagttt	1320
ggtccgcac	tggctggtgc	tcccctctca	accctgcgga	attgggagcg	tgaatttgca	1380
acttgggcac	ctcaaataga	tgttgtaaatg	tattttggag	ctgctgcttc	tcgtgacatt	1440
attaggaagt	acgagtttta	ctacccaaaa	gagaaactga	agaagctgaa	gaaaaagaaa	1500
tcttctccat	ctaatgaaga	taagaagcag	tcaaggataa	gatttgatgt	cttattgacg	1560
tcttatgaga	tgatcaacat	ggactcgtct	attctaaaaa	atatagaatg	ggagtgcctg	1620
gttggtggtg	aggggcatcg	gttgaaaaac	aaagattcca	agttgtttgg	tcaacttaaa	1680
gattataata	ccaaacatcg	tgttctatta	acggggaccc	cagtccagaa	taatcttgat	1740
gagcttttca	tgcttatgca	cttccttgag	ggtgaaaagt	ttgggagtat	aactgatctc	1800
caagaagagt	tcaaggatat	aaaccaagac	aagcaaattg	agaagcttca	tggaatgctg	1860
aagccacatc	ttcttcgaag	attcaagaag	gatgttatga	aagaacttcc	tccaaaaaag	1920
gaattgattc	tacgagttga	attgacaaga	aaacagaagg	agtactataa	ggcaattctc	1980
accaagaatt	atgaagtgtt	agcccgtcgt	aatggtggac	atacatctct	aataaacgtt	2040
gtaatggagt	tgcgcaaact	ctgttgccat	ggattcatga	ttgatgaacc	tgatcttgaa	2100
cctgccaatc	cagaagaagg	tttaaggagg	cttctagatt	catcaggtaa	gatgcagctg	2160
ctggacaaga	tgatggtgaa	actgaaagag	cagggtcata	gagttcta	ttattcacag	2220
ttccagcaca	tggtggactt	gctggaggac	tatttaagtt	acaggaaatg	gacttatgaa	2280
cgcacgatg	gcaagataag	tggcgcgtgat	aggcagatac	ggatagatcg	cttcaacgct	2340
aagaattcaa	ctaggttttg	ctttcttctt	tctactagag	ctggtggtct	gggaataaac	2400
ttggcaactg	cagatactgt	aatcatctat	gacagtgatt	ggaaccacac	tgcggatttg	2460
caagctatgg	caagagctca	tgccttagga	cagactagta	aggtgatgat	atacaggctt	2520
gtagccgag	gtacaattga	ggagcgaatg	atgcagctta	caaaaaagaa	gattttattg	2580
gagcacttag	ttgttggtcg	actcaccaaa	gctaataatg	tcaatcagga	ggagtggatg	2640
gatattatac	gctatggatc	aaaggagcct	tttgaagacg	agaatgatga	atctcgccaa	2700

attcattatg	acgaagctgc	aattgagagg	ttgttagacc	gtgatcaagt	tgacggtgat	2760
gaatctgtgg	aagatgaaga	agaagatgga	ttcttaaaaag	gattcaaggt	tgcaaaccttt	2820
gaatatatcg	atgaggcaaa	ggctcaggca	gaaaaagagg	aggcacggag	aaaggctgca	2880
gctgaggctg	aaaatttctga	aagaaactac	tgggatgaac	tattgaagga	tagatatgat	2940
gtacagaaaag	ttgaagaaca	tactgctatg	ggaaaaggga	aaagaagccg	caaacagatg	3000
gctgccgctg	atgaagatga	cattcatgat	ttaagttccg	aagatgagga	ttactcattg	3060
gaggatgaca	tttcagataa	tgacacaagt	ttgcaaggaa	atatttctgg	gaagagggga	3120
caatattcta	agagaaaatc	acgtaatgtt	gattctattc	cattgatgga	gggcgaagga	3180
cgtaccttga	gagttcttgg	attcaaccat	gctcaacgag	caatgttcct	acagacactc	3240
aatagattcg	gttttcagaa	ttatgactgg	aaagagtatc	ttcctcgtct	taaaggaaaa	3300
agtgtcgagg	aaatccagag	atatgctgaa	cttgtcatgg	cacatcttgt	tgaagaaatt	3360
aatgattctg	actatTTTTT	agatggcggt	ccaaaaggaaa	tgatgcgtgt	tgatgatgta	3420
ctagtcagga	tagcaaacat	atccccttatc	gaggagaaga	tggctgccac	aggaccagga	3480
aaaattacaa	acatTTTTT	taattacttg	ctctatgagt	tccaaggcctt	atctggtgga	3540
agaatatgga	aagcggagca	tgatctactg	ttactgagag	gcatactgaa	gcatggatat	3600
gcaaggtggc	agtatatatc	agatgacaga	gagaatgggc	tttttgaggc	tgacgacga	3660
gagctgcac	tcccttcggt	taatgaaata	attggtgctc	agttgaacga	ggcaaatggg	3720
aatttggaag	gtgcacagga	aggccaagcg	aacacaacaa	gcatgtcgca	ttacaaggag	3780
atccagagaa	agatagttga	gttcttgaga	aagagatatc	atcttatgga	gagagccttg	3840
aatctggaat	atgctgtgat	aaagaaaaaa	attcctgttc	ctgatgatat	tactgaacaa	3900
ggtgttccag	caggacatgc	tccgcttatt	ccagatatca	gtgaactgtt	gcgggaattg	3960
cccaatcttg	agccaatttc	taccaatgaa	ttgatttctg	agggcacagc	tggtcagtta	4020
caagttcccc	atctctacaa	taagatgtgt	ggagtgcctg	aagagagtgg	tgcttatgcg	4080
ctcagttcct	tctttggaga	caagtccgca	tcttctactt	tggccaatag	ccttcgacag	4140
tttgaaactg	tgtgtgagaa	tgtcgtcgag	gccttacgac	cacaccaaaa	tggtactgcc	4200
agtgccatca	aagaggaatt	ggtagatgca	gccaccaaaag	cagcagcagc	agcagctcct	4260
caacaagatt	caggccatga	tgaccgcat	gggcagtctt	cgacagccaa	ggcggacatg	4320
gaaatcgatg	gttgatttgt	aggttccaga	gtggcaagaa	agggaatccc	ctctaatacat	4380
tatgtatact	gtggtcagaa	tgtccgctat	atattgtaac	atcaaagaaa	gcacctccag	4440
gcctgagggg	gttactgcta	atgcgttttg	tttacttgtc	cttgtaatat	gcatacacat	4500
ttagaactca	tgacagccatt	gtgtgaaaaa	aaaaaaaaaa	aaaaaaaaaa	a	4551

<210> 43
 <211> 1358
 <212> PRT
 <213> Zea mays

<400> 43

Met	Ser	Ser	Leu	Val	Glu	Arg	Leu	Arg	Val	Arg	Ser	Glu	Arg	Arg	Pro
1				5					10					15	
Arg	Tyr	Ala	Leu	Asp	Glu	Ser	Asp	Asp	Asp	Leu	Pro	Leu	Arg	Val	Gly
			20					25					30		
Ala	Gly	Lys	Gly	Lys	Asp	Gln	Gln	Asn	Asp	Ala	Pro	Ala	Glu	Arg	Ile
		35					40					45			
Glu	Arg	Glu	Asp	Ala	Lys	Glu	Glu	Ala	Cys	Gln	Arg	Cys	Gly	Lys	Ser
		50					55				60				
Asp	Asn	Leu	Val	Ser	Cys	Ser	Thr	Cys	Thr	Tyr	Lys	Phe	His	Arg	Lys
65					70					75				80	
Cys	Leu	Val	Pro	Cys	Leu	Asn	Ile	Thr	Ser	Asp	Lys	Trp	Ser	Cys	Pro
			85						90					95	
Glu	Cys	Val	Ser	Pro	Leu	Thr	Tyr	Met	Glu	Arg	Ile	Leu	Asp	Ile	Glu
		100						105					110		
Val	Leu	Glu	Ala	Pro	Arg	Glu	Asp	Ser	Ser	Ser	Thr	Glu	Pro	Arg	Ser
		115					120						125		
Lys	Lys	Met	Glu	Arg	Tyr	Leu	Ile	Lys	Trp	Lys	Gly	Leu	Ser	Tyr	Ile
	130						135					140			